

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:35 : Search time 14.2364 Seconds  
(without alignments)  
1276.267 Million cell updates/sec

Title: US-09-658-699-2  
Perfect score: 1004  
Sequence: 1 MLGSRVWLMLLLPPTAQR.....QAFVAARVFAHGAAATLSP 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	10.0	204	1 FQHUGL	granulocyte colony
2	99.5	9.9	194	2 T09255	granulocyte colony
3	91	9.1	208	1 S29549	interleukin-6 - sh
4	90.5	9.0	174	2 T10268	granulocyte colony
5	88.5	8.8	207	2 A24573	granulocyte colony
6	87.5	8.7	208	2 A26496	granulocyte colony
7	86	8.6	1121	2 A82809	exodeoxyribonuclea
8	85	8.5	211	1 ICM56	interleukin-6 prec
9	80.5	8.0	232	2 D70537	hypothetical prote
10	80.5	8.0	530	2 D96810	hypothetical prote
11	80	8.0	858	2 JC7683	taste receptor T1R
12	79.5	7.9	201	2 A42247	myelomonocytic gro
13	79	7.9	506	2 AG0893	aerotoxis receptor
14	79	7.9	2512	1 XYC4FA	enoyl-lacyl-carrie
15	78	7.8	1026	2 T05882	hypothetical prote
16	77.5	7.7	513	2 C82366	conserved hypothet
17	77.5	7.7	967	2 G86229	hypothetical prote
18	76.5	7.6	399	2 A11929	N-acetyl-glucosami
19	76.5	7.6	881	2 F84404	valyl-trna synthet
20	76	7.6	262	2 A84240	molybdopterin oxid
21	75.5	7.5	214	2 JC5043	granulocyte colony
22	75.5	7.5	265	2 B83395	probable enoyl-CoA
23	75.5	7.5	938	2 A56731	chromatin assembly
24	75.5	7.5	2304	2 T07920	probable acetyl-Co
25	75	7.5	195	2 T40700	interferon omega -
26	75	7.5	211	2 A34247	interleukin-6 prec
27	75	7.5	801	1 S00943	glucose dehydrogen
28	75	7.5	975	2 T48107	hypothetical prote
29	74.5	7.4	212	2 I46621	pinterleukin 6 -

30	74.5	7.4	212	2 I46590	interleukin 6 - pi
31	74.5	7.4	280	2 S75845	hypothetical prote
32	74	7.4	314	2 T27137	hypothetical prote
33	74	7.4	2	T26739	hypothetical prote
34	74	7.4	974	2 A86263	F13K23.18 protein
35	74	7.4	2	AD0198	transcription-repa
36	73.5	7.3	247	2 H70916	probable glucose-6
37	73.5	7.3	310	2 B90696	probable glutamina
38	73.5	7.3	310	2 F85546	probable glutamina
39	73.5	7.3	649	2 T04005	probable protein k
40	73.5	7.3	755	2 D75598	photoreceptor - De
41	73.5	7.3	1015	2 I39697	beta-galactosidase
42	73	7.3	346	2 A58583	testosterone-resis
43	73	7.3	462	2 AI2319	UDP-N-acetylmutamo
44	72.5	7.2	259	2 T28147	class II histocomp
45	72.5	7.2	374	2 C98215	oligopeptide ABC t

ALIGNMENTS

RESULT 1  
FQHUGL  
granulocyte colony-stimulating factor precursor - human  
N:Alternate names: colony-stimulating factor 3; G-CSF  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1988 #sequence\_revision 18-Aug-1995 #text\_change 22-Jun-1999  
C:Accession: A25093; A49796; A47587; S68331  
R:Nagata, S.; Tsuchiya, M.; Asano, S.; Yamamoto, O.; Hirata, Y.; Kubota, N.; Oheda, M  
EMBO J. 5, 575-581, 1986  
A:Title: The chromosomal gene structure and two mRNAs for human granulocyte colony-st  
A:Reference number: A25093; MUID:86220137; PMID:2423327  
A:Accession: A25093  
A:Molecule type: DNA; mRNA  
A:Residues: 1-204 <NAG>  
A:Cross-references: EMBL:X03656; EMBL:X03655; NID:G31693; PIDN:CAA27290.1; PID:G73276  
R:Devlin, J.J.; Devlin, P.E.; Myambo, K.; Lilly, M.B.; Rado, T.A.; Warren, M.K.  
J. Leukoc. Biol. 41, 302-306, 1987  
A:Title: Expression of granulocyte colony-stimulating factor by human cell lines.  
A:Reference number: A49796; MUID:87196936; PMID:3494801  
A:Accession: A49796  
A:Molecule type: mRNA  
A:Residues: 1-204 <DEV>  
A:Cross-references: GB:M17706; NID:G183040; PIDN:AAA35882.1; PID:G183041  
R:Souza, L.M.; Boone, T.C.; Gabrilove, J.; Lai, P.H.; Zsebo, K.M.; Muddock, D.C.; Cha  
Science 232, 61-65, 1986  
A:Title: Recombinant human granulocyte colony-stimulating factor: effects  
A:Reference number: A47587; MUID:86151684; PMID:2420009  
A:Accession: A47587  
A:Molecule type: mRNA  
A:Residues: 19-204 <SOU>  
A:Cross-references: GB:M13008; NID:G183044; PIDN:AAA03056.1; PID:G183045  
R:Haniu, M.; Horan, T.; Arakawa, T.; Le, J.; Katta, V.; Rohde, M.F.  
Arch. Biochem. Biophys. 324, 344-356, 1995  
A:Title: Extracellular domain of granulocyte-colony stimulating factor receptor.  
A:Reference number: S68331; MUID:96132662; PMID:8554326  
A:Accession: S68331  
A:Molecule type: protein  
A:Residues: 1-31-46 <HAN>  
C:Genetics:  
A:Gene: GDB:CSF3  
A:Cross-references: GDB:I19083; OMIM:138970  
A:Map position: 17q11.2-17q12  
A:Introns: 14/1; 65/3; 101/3; 150/3  
C:Function:  
A:Description: stimulates the differentiation and proliferation of hematopoietic prog  
C:Superfamily: Interleukin-6  
C:Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-204/Product: granulocyte colony-stimulating factor #status predicted <MAT>  
F:66-72, 94-104/Disulfide bonds: #status predicted

Query Match 10.0%; Score 100; DB 1; Length 204;  
Best Local Similarity 25.9%; Pred. No. 0.052;  
Matches 51; Conservative 20; Mismatches 76; Indels 50; Gaps 11;

QY 15 WTAQGRAVPGSSPAWTQ-----CQO-----LSQKLTCLAWSAHP-----LVGHM 54  
||| ||| : : : : : ||| ||| : : : : :  
Db 25 WTQVQ-EATPLGPASSLSPLKLCLEQVRKIQGDGAALQELKCATYKLCHPPELVLLGH- 82  
||| ||| : : : : : ||| ||| : : : : :  
QY 55 DLREEGDETTNDVPHIQCGDCDPOGLRDNDSQFCLORIHQGLLFYKELGSDIFTG-EP 113  
||| ||| : : : : : ||| ||| : : : : :  
Db 83 -----SLGIPWAPL-SSCPQALQ--LAGLSQLHSGFLYQGLL--QALGEGISP 127  
||| ||| : : : : : ||| ||| : : : : :  
QY 114 SLPLDSPAQLHASLLGLSOLLQPGHHWETQOIPSPSPQ-----PWQRLLRFRKI 165  
||| ||| : : : : : ||| ||| : : : : :  
Db 128 ELGFTDTTLQLDVADFATTIWOQME-----ELGMAPALQPTQGAMPAPAFORRAGGVILV 183  
||| ||| : : : : : ||| ||| : : : : :  
QY 166 LRSLOAFVAAARVFAH 182  
||| ||| : : : : : ||| ||| : : : : :  
Db 184 ASHQSFLEVSRYVLRH 200  
||| ||| : : : : : ||| ||| : : : : :  
RESULT 2  
T09255  
granulocyte colony-stimulating factor precursor - cat (fragment)  
C:Species: Felis silvestris catus (domestic cat)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 20-Jun-2000  
C:Accession: T09255  
R:Dunham, S.P.; Onions, D.E.  
submitted to the EMBL Data Library, September 1996  
A:Description: Cloning, sequence and expression of feline granulocyte colony stimulating  
A:Reference number: Z16630  
A:Accession: T09255  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-194 <DUN>  
A:Cross-references: EMBL:Y08558  
C:Function:  
A:Description: stimulates the differentiation and proliferation of hematopoietic progenit  
C:Superfamily: interleukin-6  
C:Keywords: cytokine; growth factor; macrophage  
F:1-20/Domain: signal sequence (fragment) #status predicted <SIG>  
F:21-194/Product: granulocyte colony-stimulating factor #status predicted <MAT>  
Query Match 9.9%; Score 99.5; DB 2; Length 194;  
Best Local Similarity 23.9%; Pred. No. 0.054;  
Matches 50; Conservative 27; Mismatches 79; Indels 53; Gaps 11;

QY 7 VMLLLLPWTAQ-----GRAVPGSSPAWTQ-----CQO-----LSQKLTCLAWS 46  
||| ||| : : : : : ||| ||| : : : : :  
Db 2 LMAQLLLWHSALMMVQVATPLGPTSSLPQSFLLKCLEQVRKVQADGTALQERLCAHKL 61  
||| ||| : : : : : ||| ||| : : : : :  
QY 47 AHP-----LVGHMDLREEGDEETNDVPHIQCGDCDPOGLRDNDSQFCLORIHQGLLFYK 102  
||| ||| : : : : : ||| ||| : : : : :  
Db 62 CHPEELVLLGH-----ALGIPQAPL-SSCSQALQLTG--CLROLHSGFLYQ 107  
||| ||| : : : : : ||| ||| : : : : :  
QY 103 LLAGSDIFTG-EPSSLPSVAQLHASLLGLSOLLQPGHHWETQOIPSPSPQ-----154  
||| ||| : : : : : ||| ||| : : : : :  
Db 108 LL--QALAGISPELPTLDMQLDITDPAINIWOQME-----DVGMAPAVPTQTGTPTFT 161  
||| ||| : : : : : ||| ||| : : : : :  
QY 155 -PWQRLLRFRKILRSLOAFVAAARVFAH 182  
||| ||| : : : : : ||| ||| : : : : :  
Db 162 SAFQRRAGGTIVASNLQSFLEVAYRALRH 190  
||| ||| : : : : : ||| ||| : : : : :  
RESULT 3  
S29549  
interleukin-6 - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S29549  
R:Ebrahim, B.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S29549

A:Accession: S29549  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-208 <EBR>  
A:Cross-references: EMBL:X68723  
C:Superfamily: interleukin-6  
Query Match 9.1%; Score 91; DB 1; Length 208;  
Best Local Similarity 24.8%; Pred. No. 0.37;  
Matches 50; Conservative 25; Mismatches 87; Indels 40; Gaps 8;

QY 6 AVMLLLLPWTAQGRAVPGSSPAWTQCOQLSOKLCTLAWSAHPVLGHM-----DL 56  
||| ||| : : : : : ||| ||| : : : : :  
Db 13 AVSLGILLVMTS-AFTPGPLGEDFKNDTTPSRLLLTTPKEKTEALIKHIVDKISAIRKEI 71  
||| ||| : : : : : ||| ||| : : : : :  
QY 57 REGGDE-----ETTNDVPHIQCGDCDPOGLRDNDSQFCLORIHQGLLFYKELG-- 105  
||| ||| : : : : : ||| ||| : : : : :  
Db 72 CEKNDCEKSKETLAENKLLPKMEKDGCFQSGF--NOAVCLIKTTAGLLEYQIYLDLFL 129  
||| ||| : : : : : ||| ||| : : : : :  
QY 106 SDIFTGEPSSLPSVAQLHASLLGLSOLLQ-----PEGHHWETQOIPSPSPQPW 156  
||| ||| : : : : : ||| ||| : : : : :  
Db 130 ONEFEGN-----QETVMELOSSIRTLIOILKEKTAGLITTPATH---TDLLEKMQSSNEW 181  
||| ||| : : : : : ||| ||| : : : : :  
QY 157 QRLLRFRKILRSLOAFVAAAR 178  
||| ||| : : : : : ||| ||| : : : : :  
Db 182 VKNAKVILIRLSLENFLQFRLR 203  
||| ||| : : : : : ||| ||| : : : : :  
RESULT 4  
T10268  
granulocyte colony-stimulating factor - sheep (fragment)  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: T10268  
R:O'Brien, P.M.; Seow, H.F.; Rothel, J.S.; Wood, P.R.  
DNA Seq. 4; 339-342, 1994  
A:Title: Cloning and sequencing of an ovine granulocyte colony-stimulating factor cDN  
A:Reference number: Z17009; MUID:95102116; PMID:7528579  
A:Accession: T10268  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-174 <OBR>  
A:Cross-references: EMBL:L07939; NID:g310381; PIDN:AAA68006.1; PID:g310382  
C:Genetics:  
A:Gene: CSF  
C:Function:  
A:Description: stimulates the differentiation and proliferation of hematopoietic prog  
C:Superfamily: interleukin-6  
C:Keywords: cytokine; growth factor; macrophage  
Query Match 9.0%; Score 90.5; DB 2; Length 174;  
Best Local Similarity 25.5%; Pred. No. 0.33;  
Matches 40; Conservative 20; Mismatches 64; Indels 33; Gaps 8;

QY 35 QLSQKLTCLAWSAHP-----LVGHMDLREEGDEETNDVPHIQCGDCDPOGLRDNDSQFCL 90  
||| ||| : : : : : ||| ||| : : : : :  
Db 30 ELQERLCATHKLCHPPELVLLGH-----SLGIPQAPL-SSCSQSLQLTG--CL 75  
||| ||| : : : : : ||| ||| : : : : :  
QY 91 QRHQGLLFYKELGSDIFTG-EPSSLPSVAQLHASLLGLSOLLQPGHHWETQOIPS 149  
||| ||| : : : : : ||| ||| : : : : :  
Db 76 DQHLHGLFLYQGLL--QALAGISPELPTLQLDVDFATNIWQME----DLGVAPA 129  
||| ||| : : : : : ||| ||| : : : : :  
QY 150 LSPSQ-----PWQRLLRFRKILRSLOAFVAAAR 178  
||| ||| : : : : : ||| ||| : : : : :  
Db 130 VOPTQGTMTPTTSFQRRAGGVILVASQLQRFGLGLAYR 166  
||| ||| : : : : : ||| ||| : : : : :  
RESULT 5  
A24573  
granulocyte colony-stimulating factor precursor variant splice form CHU-2 - human  
N:Alternate names: colony-stimulating factor 3; G-CSF  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 16-Jul-1999

C;Accession: A24573  
R;Nagata, S.; Tsuchiya, M.; Asano, S.; Kaziro, Y.; Yamazaki, T.; Yamamoto, O.; Hirata, Y.  
Nature 319, 415-418, 1986  
A;Title: Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor.  
A;Reference number: A24573; MUID:86118679; PMID:3484805  
A;Accession: A24573  
A;Molecule type: mRNA  
A;Residues: 1-207 <NAG>  
A;Cross-references: EMBL:X03438; NID:g31689; PIDN:CAA27168.1; PID:g31690  
C;Comment: This variant splice form is not expressed in three other cell lines and may have a different function.  
C;Genetics:  
A;Gene: GDB:CSF3  
A;Cross-references: GDB:119083; OMIM:138970  
A;Map position: 17q11.2-17q12  
A;Introns: 14/1; 68/3; 104/3; 153/3  
C;Superfamily: interleukin-6  
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-207/Product: granulocyte colony-stimulating factor variant splice form CHU-2 #status predicted  
F;69-75,97-107/Disulfide bonds: #status predicted

Query Match 8.8%; Score 88.5; DB 2; Length 207;  
Best Local Similarity 25.5%; Pred. No. 0.63;  
Matches 51; Conservative 20; Mismatches 76; Indels 53; Gaps 12;

QY 15 WTAGRAVPGGSPAWTQ-----CQQ-----LSOKL---CTLAWSAHP-----LV 51  
DB 25 WTQV-BATPLGPASSLPQSFLKLEQVRKIQGDGAALQBEKLVSECATYKLCHPPELVLL 83  
QY 52 GHMDLREGDEETNDVPHIQCGDCGDPQGLRDNSSQFCQRIHQGLIFVEKILGSDIFTG 111  
DB 84 GH-----SLGIPWAPL-SSCPQALQ--LACCLSQLHSGFLYQGLL--QALRG 127  
QY 112 -EPSLLPDSFVPAQLHASLLGLSQLLOPEGHWHWTQQTPLSPSQ-----PWQLLLR 162  
DB 128 ISPELGPTLDTQLDQVADFATTIWOOME-----ELGMAPALQPTQGMAPAFASAFORRAG 183  
QY 163 FKILRSLOAFVAAARVFAH 182  
DB 184 VLVASHLQSGFLEVSRYLRH 203

RESULT 6  
A26496  
granulocyte colony-stimulating factor precursor - mouse  
N;Alternate names: G-CSF  
C;Species: Mus musculus (house mouse)  
C;Date: 05-Oct-1988 #sequence\_revision 05-Oct-1988 #text\_change 16-Jul-1999  
C;Accession: A29536; A26496; S02493  
R;Tsuchiya, M.; Kaziro, Y.; Nagata, S.  
Eur. J. Biochem. 165, 7-12, 1987  
A;Title: The chromosomal gene structure for murine granulocyte colony-stimulating factor.  
A;Reference number: A29536; MUID:87190474; PMID:3494605  
A;Accession: A29536  
A;Molecule type: DNA  
A;Residues: 1-208 <TSU>  
A;Cross-references: GB:X05402; NID:g51059; PIDN:CAA28986.1; PID:g51060  
R;Tsuchiya, M.; Asano, S.; Kaziro, Y.; Nagata, S.  
Proc. Natl. Acad. Sci. U.S.A. 83, 7633-7637, 1986  
A;Title: Isolation and characterization of the cDNA for murine granulocyte colony-stimulating factor.  
A;Reference number: A26496; MUID:87017003; PMID:3489940  
A;Accession: A26496  
A;Molecule type: mRNA  
A;Residues: 1-208 <TSU>  
A;Cross-references: GB:M13926; NID:g193451; PIDN:AAA37672.1; PID:g309248  
R;Simpson, R.J.; Nice, E.C.; Nicola, N.A.  
Biol. Chem. Hoppe-Seyler 368, 1327-1331, 1987  
A;Title: Structural studies on the murine granulocyte colony-stimulating factor.  
A;Reference number: S02493; MUID:88106998; PMID:3501294  
A;Accession: S02493  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 31-34,'X',36-43;48-51,'X',53-57,'X',60-71;159-164,'X',166-176;183-198,'X',20

C;Genetics:  
A;Introns: 14/1; 71/3; 107/3; 156/3  
C;Superfamily: interleukin-6  
C;Keywords: cytokine; growth factor; macrophage; monomer

Query Match 8.7%; Score 87.5; DB 2; Length 208;  
Best Local Similarity 25.0%; Pred. No. 0.78;  
Matches 41; Conservative 23; Mismatches 59; Indels 41; Gaps 10;

QY 36 LSOKLCTLAWSAHP-----LVGHMDLREBDEETNDVPHIQCGDCGDPQGLRDNSSQFCLO 91  
DB 67 LLEQLCATYKLCHPPELVLLGH-----SLGIPKASL-SGCSQALQQTQ--CUS 112  
QY 92 RIHQGLIFVEKILGSDIFTG-EPSLLPDSFVPAQLHAS-----LIGLSQLQPRG 139  
DB 113 QLHSGCLYQGLL--QALSGISPALAPTDLQLDQVADFATTIWOQMENLGVAPTQVP-- 168  
QY 140 HHWTQQTPLSPSPQWQRLKILRSLOAFVAAARVFAH 182  
DB 169 ---TUSAMPAP TSA--FORRAGGVLAISYLOGFLETARLALHH 206

RESULT 7  
A82809  
exodeoxyribonuclease V gamma chain XF0422 [imported] - Xylella fastidiosa (strain 9a5  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: A82809  
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Se  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: A82809  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1121 <STM>  
A;Cross-references: GB:AE003893; GB:AE003849; NID:g9105253; PIDN:AAF83232.1; GSPDB:G  
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.E.A.; Carraro, D.M.; Carrel  
as-Neto, E.; Docena, C.; El-Dorfi, H.; Paciniani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; F  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; L  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins  
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Imieri,  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli,  
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L  
A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF0422

Query Match 8.6%; Score 86; DB 2; Length 1121;  
Best Local Similarity 23.7%; Pred. No. 8;  
Matches 41; Conservative 18; Mismatches 56; Indels 58; Gaps 9;

QY 22 VPGSSPANTQQQLSOKL-----CTL-----AWSA-----HPLVGHMDLREGDE 62  
DB 236 LPTTKEYWGAQPTQRLHQPTDCVTQTGENRLHAWGAAGRDFMTVLGSEYEVHPSGE 295  
QY 63 ETTNDVPHIQCGDCGDPQGLRDNSSQFCQRIHQGLIFVEKILGSDIFTG---PSLLP- 117  
DB 296 ITAYDDPEQRGLTTLDEGLRDS---LLQRMH-----ADLFHNSAPVAPLPA 341  
QY 118 ---DSPVAQLHASLLGLSOLL-----QPEGHWHWTQQTPLSPSQ 154  
DB 342 PRLEDPESLOFHACHTRLRELQVLHDLRLALLEPNSPEGRFN-----PPLQPRE 390

RESULT 8

ICM56

interleukin-6 precursor - mouse

N;Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte acytoma growth factor

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 sequence,revision 30-Jun-1990 #text.change 22-Jun-1999

C:Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S1C

R;Tanabe, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.

J. Immunol. 141, 3875-3881, 1988

A;Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential

A;Reference number: A30531; MUID:89035525; PMID:3263439

A;Accession: A30531

A;Molecule type: DNA

A;Residues: 1-211 <TAN>

A;Cross-references: GB:M20572; NID:q198369; PIDN:AAA39302.1; PID:g387386

R;Van Snick, J.; Gayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim

Eur. J. Immunol. 18, 193-197, 1988

A;Title: cDNA cloning of murine interleukin-HPL: homology with human interleukin 6.

A;Reference number: A27610; MUID:88166883; PMID:2965020

A;Accession: A27610

A;Molecule type: mRNA

A;Residues: 1-211 <VAN>

A;Cross-references: GB:X06203; NID:g52701; PIDN:CAA295560.1; PID:g52702

R;Wock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla

J. Immunol. 142, 1372-1376, 1989

A;Title: The murine IL-6 gene maps to the proximal region of chromosome 5.

A;Reference number: A30571; MUID:89124383; PMID:2563387

A;Accession: A30571

A;Molecule type: mRNA

A;Residues: 5-211 <MOG>

A;Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699

R;Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.

Eur. J. Biochem. 176, 187-197, 1988

A;Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and

A;Reference number: S01323; MUID:88329059; PMID:3262059

A;Accession: S01323

A;Molecule type: protein

A;Residues: 25-166,'X',168-211 <SIM>

A;Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A

R;Gronett, H.E.; Fuentes, N.L.; Fuller, G.M.

Nucleic Acids Res. 18, 6455, 1990

A;Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.

A;Reference number: S12103; MUID:91057159; PMID:2243807

A;Accession: S12103

A;Molecule type: mRNA

A;Residues: 1-211 <GRE>

A;Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728

R;Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.

Biochem. Biophys. Res. Commun. 166, 139-145, 1990

A;Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage

A;Reference number: A90157; MUID:90147691; PMID:2302197

A;Accession: E34047

A;Molecule type: protein

A;Residues: 56-69,'X',71-75;78-94;128-148 <JAS>

R;Van Snick, J.; Gayphas, S.; Vink, A.; Uyttendhoe, C.; Coullie, P.G.; Rubira, M.R.; Sim

Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986

A;Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokin

A;Reference number: A26662; MUID:87092311; PMID:2948184

A;Accession: A26662

A;Molecule type: protein

A;Residues: 25-39,'X',41-42,'X',44-45 <VSN>

R;Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.

Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988

A;Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone

A;Reference number: A40486; MUID:89017145; PMID:3262872

A;Accession: A40486

A;Molecule type: mRNA

A;Residues: 1-211 <CHI>

A;Cross-references: GB:J03783; NID:q198367; PIDN:AAA39301.1; PID:g309410

R;Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S

Blood 72, 2070-2073, 1988

A;Title: The ryevidel blood cell differentiation-inducing protein MGI-2A is interleukin-

A:Reference number: A60799; MUID:89062753; PMID:3264198

A:Accession: A60799

A:Molecule type: protein

A:Residues: 77-98 <SHA>

R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.

J. Exp. Med. 171, 965-970, 1990

A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a

A:Reference number: S10241; MUID:90171860; PMID:2106569

A:Accession: S10241

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-6 <BLA>

A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860

R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.

Eur. J. Biochem. 217, 53-59, 1993

A:Title: Specific covalent modification of the tryptophan residues in murine interleukin

A:Reference number: S38254; MUID:94039075; PMID:8223586

A:Accession: S38254

A>Status: preliminary

A:Molecule type: protein

A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZHA>

C:Genetics:

A:Gene: IL-6

A:Map position: 5

A:Introns: 7/1; 68/3; 106/3; 156/3

C:Superfamily: interleukin-6

C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-211/Product: interleukin-6 #status experimental <MAT>

Query Match Score 85; DB 1; Length 211;  
Best Local Similarity 22.9%; Pred. No. 1.4;  
Matches 44; Conservative 20; Mismatches 58; Indels 70; Gaps 9;

QY 28 PAWTCQ-----OLSKKLTAWSAHPLVGHMDLRREGDEETND--VPHIQ 72  
          |||               :::||||               |-:-|||  
Db 44 PVYTSQVGLITHVLWEIVEMRKELCN-----GNSDCMNDALAEENKLPEIQ 94  
          |||               :::||||               |-:-|||

QY 73 CGDGDPOGLRDNOSFCLOTHOGLIFYE-----KLGSD-----I 108  
          |||               :::||||               |-:-|||

Db 95 RNDGCQTGTGY--NQBIKLTIKSSGLFYSLEYVMKNLNKDKNKARVLQRDTFTLLHI 152  
          |||               :::||||               |-:-|||

QY 109 FTGPESLLDPSPVAQLHASLL--GLSQILOPGEHHWFETOQIPSLSPSQWRLLLLRFKIL 166  
          |||               :::||||               |-:-|||

Db 153 FNQE-----VKDLHKIVLPTPTSNAALLTD-----KLESQKEWLTKTIQFIL 194  
          |||               :::||||               |-:-|||

QY 167 RSLQAFVAVAR 178  
          |||               :::||||               |-:-|||

Db 195 KSLEEFKVTCLR 206  
          |||               :::||||               |-:-|||

RESULT 9

D70537

hypothetical protein Rv1115 - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C:Accession: D70537

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon

& Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,

Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70537

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-232 <COL>

A:Cross-references: GB:295585; GB:AL123456; NID:g3261787; PIDN:CAB09047.1; PID:e31713

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv1115

```
Query Match      8.0%; Score 80.5; DB 2; Length 232;
Best Local Similarity 23.4%; Pred. No. 4;
Matches 49; Conservative 27; Mismatches 68; Indels 65; Gaps 11;

QY 9 LLLLPWTAQGRAVPGGSPAWTQCQQLSOKLCTLAWSAHPVLGHMDLREEGDE----- 63
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 26 LITLINQVGPYPYIPGDSPTAGTDCSELASWVSNA-TARPVFG--DRENTGNEEAALAA 82
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 64 -----TTNDVPHIQCGDCDPOGLRDNSQFCLQRIHQGLIFYEKLGLSDIFTGEP--- 100
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 83 RGFOQGTAPNALVIGWNGHHHTAVTLPDGTPTVSSGEG---GGVRVGG---GGAYPKFTH 135
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 101 EKILGSDIFTGR---PSLLPDSVAQLHASLLGLSOLQLOPEGHWHWTQOIPSLSPSQ--- 154
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 136 HMYLPMVDVAGEDQPPA--PDEPVTAVDD-----VEPE-----MPAPCTQRP 177
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 155 --PWQELLRLRKIL-RSLOAFVAVAARVF 180
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 178 VTRHNLCKNLRTMPGALSAAALAAAPVW 206
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 10
D96810
hypothetical protein Tl111.6 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D96810
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: D96810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-530 <STO>
A:Cross-references: GB:AE005173; NID:96587860; PIDN:AAF18546.1; GSPDB:GN00141
C:Genetics:
A:Gene: Tl111.6
A:Map position: 1

Query Match      8.0%; Score 80.5; DB 2; Length 530;
Best Local Similarity 25.7%; Pred. No. 11;
Matches 28; Conservative 22; Mismatches 38; Indels 21; Gaps 6;

QY 78 DPQGLR--DNSQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLDPSPV--AQLHASLLGLSQ 133
   ||| :||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 158 DPETLKMGNIEYICRGRTGQALVFYERASAD-----PKTPTYWSNKSAAALISLR 208
   ||| :||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 134 LLOPEGHWHWTQOIPSLSPSPQWRQLLRKILRSLOAFVAVAARVFAH 182
   ||| :||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 209 LLEASD--ACEEAURLNPT--YERAHOR---LASLQLRGLGEVEKALCH 249
   ||| :||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 11
JC7683
taste receptor T1R3 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 30-Sep-2001
C:Accession: JC7683
R:Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A.
Biochem. Biophys. Res. Commun. 283, 236-242, 2001
A:Title: Molecular genetic identification of a candidate receptor gene for sweet taste.
A:Reference number: JC7683; MUID:21222875; PMID:11322794
A:Contents: tongue
A:Accession: JC7683
A:Molecule type: mRNA

A:Residues: 1-858 <KIT>
A:Cross-references: DDBJ:AB049994
C:Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the
C:Genetics:
A:Gene: t1r3
A:Map position: 4
C:Keywords: transmembrane protein

Query Match      8.0%; Score 80; DB 2; Length 858;
Best Local Similarity 27.4%; Pred. No. 21;
Matches 51; Conservative 9; Mismatches 66; Indels 60; Gaps 11;

QY 3 GSRVAMLLLLLPWTAQGRAVPGGSPAWTQCQQLSOKLCTLAWSAHPVLGHMDLREEGDE 62
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 570 GEPVLSLLLL-----LCLVLGLAALAGLSVH-----HW----- 599
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 63 ETINDVPHIQCGDCDPOGLRDNSQFCLQRIHQGLIFYEKLGLSDIFTGEP---SLLPDS 119
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 600 -----DSPLVQASGG-----SQFCGICIGLCFCLSVLL-----FPGRPSSASCLAQ 642
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 120 PVAQLHASLLG--LSQLQLOPEGHWHWTQOIPSLSPSPQWRQLLRKILRSLOAFVAVAA 178
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 643 PMA--HLPLTGCGLSTFLQAAETFESELP--LS-----WANWLCSY--LRGLWAWLVLLIA 693
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 179 VFAHGA 184
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 694 TFVEAA 699
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 12
A42247
myelomonocytic growth factor precursor - chicken
N:Alternate names: colony-stimulating factor CMGF
C:Species: Gallus gallus (chicken)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: A42247; S03633
R:Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A:Title: Structure of the chicken myelomonocytic growth factor gene and specific act.
A:Reference number: A42247; MUID:92195319; PMID:1549124
A:Accession: A42247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <STE>
A:Note: sequence extracted from NCBI backbone (NCBIN:89832, NCBIP:89836)
R:Leutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.;
EMBO J. 8, 175-181, 1989
A:Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals
A:Reference number: S03633; MUID:89231616; PMID:2785450
A:Accession: S03633
A:Molecule type: mRNA
A:Residues: 1-201 <LEU>
A:Cross-references: EMBL:X14477; NID:963596; PIDN:CAA32639.1; PID:963597
C:Superfamily: interleukin-6
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-201/Product: myelomonocytic growth factor #status predicted <MAT>
F:123,137/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      7.9%; Score 79.5; DB 2; Length 201;
Best Local Similarity 28.6%; Pred. No. 4.2;
Matches 36; Conservative 19; Mismatches 52; Indels 19; Gaps 6;

QY 69 PHIQCG--DGCDDPQGLRNSQFCLQRIHQGLIFYEKLGLSDIFTGEPSSLDPDS----PVA 122
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 79 PHLVQAPLQDQCHKRGFQ--AEVCFQIIRAGLHAYHDSLGAVL-----RLLPNHTTLVETL 131
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 123 QLHASLLGLSOLQLOPEGHWHWTQOIPS--LSP-----SQPWQRLLRKILRSLOAFVAVA 176
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 132 QLDAAANLSSNIQQQMEDLGLDVTVLPAEQRPSPPTFTSGPQQQVGGFFILANFQRFLETA 191
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 177 ARVFAH 182
   ||| :||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

Db 192 YRALRH 197

## RESULT 13

AG0893

aerotoxis receptor protein [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C;Species: Salmonella enterica subsp. enterica serovar Typhimurium

A;Note: this species has also been called Salmonella typhimurium

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 17-May-2002

C;Accession: AG0893

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, M.;

S.; Mouté, S.; O'Gaora, P.

th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, C.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar

A;Reference number: AB0502; PMID:11677608

A;Accession: AG0893

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-506 &lt;PAR&gt;

A;Cross-references: GB:AL513382; PID:CAD07741.1; PID:g16504293; GSPDB:GN00176

C;Genetics:

A;Gene: STY3395

C;Superfamily: methyl-accepting chemotaxis protein

Query Match 7.9%; Score 79; DB 2; Length 506;

Best Local Similarity 21.3%; Pred. No. 14;

Matches 40; Conservative 19; Mismatches 55; Indels 74; Gaps 6;

QY 48 HPLVGHMDL-----REEGDE--ETNDVPHIQCGDGDQDPQ 80

| | | | | : | | | | | : | | | | |

Db 53 HNLVRHPDMPKAAFAADWMTLKQGPWSGIVKRNKRGDHYVRANAVPMIREGRVTGYM 112

| | | | | : | | | | | : | | | | |

QY 81 GLRD-----NSQCLQRIHOGILFYKELIGSDIFTGPELSPVQ 123

: | : | : | : | : | : | : | : | : |

Db 113 SIIRATFDDBIAVEPLYQALNEGRCRIHGLVVRQGLLQK-----LPMAPVRW 163

: | : | : | : | : | : | : | : | : |

QY 124 LHASLGLSLLQPEGHWHWETOQISLSPSPQWRLL-----RFKILRSIQ 171

: | : | : | : | : | : | : | : | : |

Db 164 RVSINGLMAMV-----LALALFGTDSQWALLLGLALAMLAGTALFEWQIVRPIEN 214

: | : | : | : | : | : | : | : | : |

QY 172 FVAVARV 179

| : | : |

Db 215 VATQALKV 222

| : | : |

## RESULT 14

XYCHFA

enoyl-[acyl-carrier-protein] reductase (NADPH2, B-specific) (EC 1.3.1.10) - chicken

N;Contains: 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61); 3-oxoad

enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.10); oleoyl-[acyl-car

protein] S-malonyltransferase (EC 2.3.1.39)

C;Species: Gallus gallus (chicken)

C;Date: 30-Sep-1991 #sequence\_revision 12-Apr-1996 #text\_change 03-Jun-2002

C;Accession: S57248; S51519; A30620; A29967; A33918; A30445; A31236; A31236; A30297; A31

R;Huang, W.Y.; Chirala, S.S.; Wakil, S.J.

submitted to the EMBL Data Library, January 1989

A;Description: Amino-terminal blocking group and sequence of the animal fatty acid synth

A;Reference number: S57248

A;Accession: S57248

A;Molecule type: mRNA

A;Residues: 1-2512 &lt;HUAL&gt;

A;Cross-references: EMBL:J04485; NID:g460908; PID:ABA46389.1; PID:g460907

R;Huang, W.Y.; Chirala, S.S.; Wakil, S.J.

Arch. Biochem. Biophys. 314, 45-49, 1994

A;Title: Amino-terminal blocking group and sequence of the animal fatty acid synthase.

A;Reference number: S51519; MUID:95031085; PMID:7944406

A;Accession: S51519

A;Molecule type: mRNA

A;Residues: 1-182 &lt;HUA2&gt;

A;Cross-references: EMBL:J04485; NID:g460908

A;Accession: A30620

A;Molecule type: protein  
 A;Residues: 1-12 <HUA3>  
 A;Note: determination of acetylated amino end  
 R;Chang, S.I.; Hammes, G.G.  
 Biochemistry 27, 4753-4760, 1988  
 A;Title: Amino acid sequences of substrate-binding sites in chicken liver fatty acid  
 A;Reference number: A29967; MUID:89000676; PMID:3167014  
 A;Accession: A29967  
 A;Molecule type: protein  
 A;Residues: 144-166;575-583;2141-2165 <CHAL>  
 R;Holzer, K.P.; Liu, W.; Hammes, G.G.  
 Proc. Natl. Acad. Sci. U.S.A. 86, 4387-4391, 1989  
 A;Title: Molecular cloning and sequencing of chicken liver fatty acid synthase cDNA.  
 A;Reference number: A33918; MUID:89282777; PMID:2734291  
 A;Accession: A33918  
 A;Molecule type: mRNA  
 A;Residues: 75-77,'PV',80-116,'A',118-675,'S',677-1169,'N',1171-1178,'T',1180-1191,'H  
 L>  
 A;Accession: A30445  
 A;Molecule type: protein  
 A;Residues: 107-113;1086-1091 <HOL1>  
 R;Yuan, Z.; Liu, W.; Hammes, G.G.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 6328-6331, 1988  
 A;Title: Molecular cloning and sequencing of DNA complementary to chicken liver fatty  
 A;Reference number: A31236; MUID:88320436; PMID:2842766  
 A;Accession: A31236  
 A;Molecule type: mRNA  
 A;Residues: 1752-2350,'CFSSFLFO',2351-2512 <YUAI>  
 A;Accession: B31236  
 A;Molecule type: mRNA  
 A;Residues: 1752-2512 <YUA2>  
 A;Cross-references: GB:J03860; GB:M22987; NID:g211766  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are s  
 R;Chirala, S.S.; Kasturi, R.; Pazirandeh, M.; Stolor, D.T.; Huang, W.Y.; Wakil, S.J.  
 J. Biol. Chem. 264, 3750-3757, 1989  
 A;Title: A novel cDNA extension procedure. Isolation of chicken fatty acid synthase c  
 A;Reference number: A30297; MUID:89139426; PMID:2917973  
 A;Accession: A30297  
 A;Molecule type: mRNA  
 A;Residues: 1568-2512 <CHI>  
 A;Cross-references: EMBL:J04485; NID:g460908  
 A;Note: neither the complete nucleic acid sequence nor the complete translation are s  
 R;Yang, C.Y.; Huang, W.Y.; Chirala, S.; Wakil, S.J.  
 Biochemistry 27, 7773-7777, 1988  
 A;Title: Complete amino acid sequence of the thioesterase domain of chicken liver fat  
 A;Reference number: A31184; MUID:89088151; PMID:3207709  
 A;Accession: A31184  
 A;Molecule type: protein  
 A;Residues: 2209-2508 <YAN>  
 R;Kasturi, R.; Chirala, S.; Pazirandeh, M.; Wakil, S.J.  
 Biochemistry 27, 7778-7785, 1988  
 A;Title: Characterization of a genomic and cDNA clone coding for the thioesterase dom  
 A;Reference number: A31185; MUID:89088152; PMID:3207710  
 A;Accession: A31185  
 A;Molecule type: DNA  
 A;Residues: 2202-2512 <KAS1>  
 A;Cross-references: EMBL:J02839; NID:g211768; PID:AAA82106.1; PID:g211769  
 A;Accession: A30446  
 A;Molecule type: mRNA  
 A;Residues: 2202-2512 <KAS2>  
 A;Cross-references: EMBL:J02839; NID:g211768  
 A;Note: the translated sequence in Genbank entry CHKFAA, release 113.0, PID:AAA8210  
 wn in Fig. 5  
 R;Huang, W.Y.; Stoops, J.K.; Wakil, S.J.  
 Arch. Biochem. Biophys. 270, 92-98, 1989  
 A;Title: Complete amino acid sequence of chicken liver acyl carrier protein derived f  
 A;Reference number: S03856; MUID:89192401; PMID:2648999  
 A;Accession: S03856  
 A;Molecule type: protein  
 A;Residues: 2121-2209 <HUA4>  
 R;Chang, S.I.; Hammes, G.G.  
 Biochemistry 28, 3781-3788, 1989  
 A;Title: Amino acid sequences of pyridoxal 5'-phosphate binding sites and fluorescenc

A:Reference number: A32015; MUID:89323081; PMID:2751995  
A:Accession: A32015  
A:Molecule type: protein  
A:Residues: 667-675;1699-1709 <CH>  
A:Note: the binding of pyridoxal 5'-phosphate to Lys-1708 competitively inhibits the binding of Lys-1709 to the protein  
C:Function: <HBD>  
A:Description: as 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.61) catalyzes the conversion of 3-hydroxypalmitoyl-[acyl-carrier-protein] to palmitoyl-[acyl-carrier-protein] and NADP+  
A:Pathway: fatty acid biosynthesis  
A:Note: this activity is specific for C12 to C16 acyl compounds  
C:Function: <OAS>  
A:Description: as 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) catalyzes the reduction of 3-oxoacyl-[acyl-carrier-protein] to acyl-[acyl-carrier-protein] and NADPH  
A:Pathway: fatty acid biosynthesis  
C:Function: <OAS>  
A:Description: as 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) catalyzes the conversion of 3-oxoacyl-[acyl-carrier-protein] to acyl-[acyl-carrier-protein] and carbon dioxide  
A:Pathway: fatty acid biosynthesis  
C:Function: <OAS>  
A:Description: as enoyl-[acyl-carrier-protein] reductase (NADPH, B-specific) (EC 1.3.1.1) catalyzes the reduction of enoyl-[acyl-carrier-protein] to acyl-[acyl-carrier-protein] and NADPH  
A:Pathway: fatty acid biosynthesis  
C:Function: <HVD>  
A:Description: as oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) catalyzes the hydrolysis of oleoyl-[acyl-carrier-protein] to acyl-[acyl-carrier-protein] and water  
A:Pathway: fatty acid biosynthesis  
C:Function: <SAT>  
A:Description: as [acyl-carrier-protein] S-acyltransferase (EC 2.3.1.38) catalyzes the transfer of an acyl group from an acyl carrier protein to a substrate  
A:Pathway: fatty acid biosynthesis  
C:Function: <SMT>  
A:Description: as [acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39) catalyzes the transfer of a malonyl group from an acyl carrier protein to a substrate  
A:Pathway: fatty acid biosynthesis  
C:Function: <SMT>  
A:Superfamily: rat fatty acid synthase; 3-oxoacyl-[acyl-carrier-protein] synthase I homolog  
A:Keywords: acetylated amino end; acyltransferase; alternative splicing; carbon-oxygen bond cleavage; oxidoreductase; phosphopantetheine; phosphoprotein; thiolester hydrolase  
F:1-2512/Product: fatty acid synthase, splice form 1 #status predicted <MAT1>  
F:1-2350/CFGSFQF,2351-2512/Product: fatty acid synthase, splice form 2 #status predicted <OASH>  
F:22-404/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OASH>  
F:492-774/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>  
F:1322-1340/Region: catalytic (of 3-hydroxypalmitoyl-[acyl-carrier-protein] dehydratase)  
F:1554-1858/Domain: long-chain alcohol dehydrogenase homology <LADH>  
F:1675-1704/Region: beta-alpha-beta NADP nucleotide-binding fold  
F:1888-2070/Domain: short-chain alcohol dehydrogenase homology <SADH>  
F:2123-2193/Domain: acyl carrier protein homology <ACP>  
F:2234-2487/Domain: oleoyl-[acyl-carrier-protein] hydrolase homology <ACPH>  
F:1/Modified site: acetylated amino end (Met) #status experimental  
F:161/Active site: Cys #link OAS #status predicted  
F:580/Active site: Ser #link SAT, SMT #status predicted  
F:1705,1708/Active site: Ser, Lys #link EAR #status predicted  
F:1930/Active site: Lys #link OAR #status predicted  
F:2158/Binding site: phosphopantetheine (Ser) (covalent) #status predicted  
F:2309/Active site: Ser #link HYD #status predicted

Query Match 7.9%; Score 79; DB 1; Length 2512;  
Best Local Similarity 23.3%; Pred. NO. 95;  
Matches 37; Conservative 23; Mismatches 51; Indels 48; Gaps 9;

QY 20 RAVPGSSPAWTCQOLSKLCTLAWSAHLVGHMDREGEETNDVPHIQCGGCDP 79  
DB 1170 KGAAAGSPAQKGLQHILIEICRLGNP---HSEL-----EQIVTQKMHQ----DDP 1218  
QY 80 --OGLRDNQF--CLQRIHQG-----LIFYEKLKGS-IFTGEPSPDPSPVAQ----- 123  
DB 1219 LLNGLDSSBLKCLDVAKENTSHRMKIVEALAGSRVRSVQILNTQLLDIYAT 1278  
QY 124 -----LHASLLGLSLOLLOPEGHWHWTQOIPS 149  
DB 1279 DCTPFLSNWETELHDAGISFQ-----WDPSLSPS 1309

RESULT 15

T05882  
hypothetical protein F6H11.10 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse ear cress)  
C:Date: 09-Apr-1999 #sequence\_revision 09-Apr-1999 #text\_change 13-Aug-1999  
C:Accession: T05882  
R:Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Bancroft, I.;  
submitted to the Protein Sequence Database, April 1998  
A:Reference number: Z15456  
A:Accession: T05882  
A:Molecule type: DNA  
A:Residues: 1-1026 <BEV>  
A:Cross-references: EMBL:AL021684  
A:Experimental source: cultivar Columbia; BAC clone F6H11  
C:Genetics:  
A:Map position: 5  
A:Introns: 37/2; 109/1; 115/2; 560/1; 737/1; 833/3  
A:Note: F6H11.10

Query Match 7.8%; Score 78; DB 2; Length 1026;  
Best Local Similarity 22.9%; Pred. NO. 41;  
Matches 30; Conservative 18; Mismatches 53; Indels 30; Gaps 3;  
QY 2 LGSRAVMLLLLPWTAAQGRAVPGSSPAWTCQOLSKLCTL-----AWSAHP 49  
DB 518 VGLAAKLLLV-----IQSGCDPALKQBSAELLKLSLHYSDSMFISKYAWLARS 567  
QY 50 LVGHMDLRE--EGDETTNDVPHIQCGGCDPQGLRDNQSFCLQRIHQGLIFYEKLKGS 107  
DB 568 IANSLKLEDEDDDKHLNQKPSSEVSQSPRGVKEDISELTKTLR-----TQFWGVA 621  
QY 108 IFTGEPSPDP 118  
DB 622 SFLSQSPSSPD 632

Search completed: November 20, 2002, 11:55:00  
Job time: 16.2364 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:59 ; Search time 7.85455 Seconds  
(without alignments)  
998.024 Million cell updates/sec

Title: US-09-658-699-2  
Perfect score: 1004  
Sequence: 1 MLGSRVAMLLLLPWTQAQR.....QAFVAAARVFAHGAATLSP 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	CSF3_PIG	106.5	10.6	195	1	002837 sus scrofa
2	CSF3_FELCA	99.5	9.9	194	1	002708 felis silve
3	IL6_SHEEP	96	9.6	208	1	P23455 ovis aries
4	CSF3_SHEEP	90.5	9.0	174	1	Q28746 ovis aries
5	CSF3_CANFA	89.5	8.9	175	1	P35834 canis famil
6	IL6_CAPHI	89	8.9	208	1	Q28319 capra hircu
7	CSF3_HUMAN	88.5	8.8	207	1	P09919 homo sapien
8	CSF3_MOUSE	87.5	8.7	208	1	P09920 mus musculu
9	IL6_MOUSE	85	8.5	211	1	P08505 mus musculu
10	CSF3_BOVIN	80.5	8.0	195	1	P35833 bos taurus
11	PR23_DROME	79.5	7.9	201	1	077438 drosophila
12	MGF_CHICK	79	7.9	2511	1	P13854 gallus gall
13	FAS_CHICK	78.5	7.8	208	1	P12276 gallus gall
14	IL6_FELCA	78.5	7.8	208	1	P41683 felis silve
15	AT10_MOUSE	77.5	7.7	450	1	P58459 mus musculu
16	RMUC_VIBCH	77.5	7.7	513	1	Q9KVG7 vibrio chol
17	CAFA_HUMAN	75.5	7.5	938	1	Q13111 homo sapien
18	IL6_ORCOR	75	7.5	205	1	Q28747 orcinus orc
19	IL6_RAT	75	7.5	211	1	P20607 rattus norv
20	DHGA_ALICA	75	7.5	801	1	P05465 acinetobact
21	IL6_PIG	74.5	7.4	212	1	P26893 sus scrofa
22	TNFB_MACEU	73.5	7.3	201	1	Q9XT48 macropus eu
23	IL6_CANFA	73.5	7.3	207	1	P41323 canis famil
24	6PGL_MYCTU	73.5	7.3	247	1	Q06814 mycobacteri
25	BPHY_DEIRA	73.5	7.3	755	1	Q9RZA4 deinoxococ
26	BGAL_ARTSP	73.5	7.3	1015	1	Q59140 arthrobacte
27	KG3H_DROME	72	7.2	501	1	P83101 drosophila
28	GLS1_ECOLI	71.5	7.1	310	1	P77454 escherichia
29	IL6_BOVIN	71	7.1	208	1	P26892 bos taurus
30	IL6_CERTO	71	7.1	212	1	P46650 cercocobus
31	KPYK_METEX	71	7.1	483	1	O05118 methylobact
32	ELF1_HUMAN	71	7.1	619	1	P32519 homo sapien
33	IND1_HUMAN	70	7.0	195	1	P37290 homo sapien

34	70	7.0	427	1	TH1L_HUMAN	P24752 homo sapien
35	70	7.0	726	1	AD20_HUMAN	O43506 homo sapien
36	70	7.0	812	1	PD41_ORYZA	Q43007 oryza sativ
37	70	7.0	1538	1	LHR_ECOLI	P30015 escherichia
38	69.5	6.9	208	1	IL6_HORSE	Q95181 equus cabal
39	69.5	6.9	430	1	KDTA_CHLMU	Q9PK55 chlamydia m
40	69.5	6.9	514	1	G6PD_MYCTU	O08407 mycobacteri
41	69.5	6.9	1396	1	VCAP_VZVD	P09245 varicella-z
42	69.5	6.9	1544	1	TUSP_HUMAN	Q9NRJ4 homo sapien
43	69	6.9	234	1	NK4_HUMAN	P24001 homo sapien
44	69	6.9	592	1	FTSZ_BARBA	O31314 bartonella
45	69	6.9	639	1	AMVG_ASPAK	P23176 aspergillus

ALIGNMENTS

RESULT 1  
CSF3\_PIG  
ID CSF3\_PIG STANDARD; PRT; 195 AA.  
AC O02837; O19180;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Granulocyte colony-stimulating factor precursor (G-CSF).  
GN CSF3.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kumburg P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RA Gloster S.E., Sandeman R.M., Strom A.D.G.;  
RT "Cloning of a cDNA and gene encoding porcine granulocyte-colony  
stimulating factor.";  
RT Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE  
CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,  
DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS  
OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS  
CSF INDUCES GRANULOCYTES (BY SIMILARITY).  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- PTM: O-GLYCOSYLATED (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; Y10494; CAA71518.1; -;  
DR EMBL; U68482; AAB70701.1; -;  
DR EMBL; U68481; AAB70700.1; -;  
DR HSSP; P35833; 1BCG.  
DR InterPro; IPR003629; GCSF\_MGF.  
DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
DR Pfam; PF00489; IL6; 1.  
DR PRINTS; PR00433; IL6GCSFMGF.  
DR PRODOM; PD008388; GCSF\_MGF; 1.  
DR SMART; SM00126; IL6; 1.  
DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal.  
FT SIGNAL 1 21 POTENTIAL.  
FT CHAIN 22 195 GRANULOCYTE COLONY-STIMULATING FACTOR.



```
DR EMBL; X62501; CAA44363.1; -.
DR EMBL; X68723; CAA48662.1; -.
DR EMBL; A19159; CAA01443.1; -.
DR PIR; S29549; S29549.
DR HSP; P05231; IL16.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 9.6%; Score 96; DB 1; Length 208;
Best Local Similarity 24.8%; Pred. No. 0.046;
Matches 50; Conservative 26; Mismatches 86; Indels 40; Gaps 8;

QY 6 AVMLLLPWAQGRAVPGSSPAWTCQQLSKLCTLAWSAHPVLVGHM-----DL 56
DQ 13 AVSLGLLVMTS-APPTGPGIGEDFNKNDTPSRLLLTTEKTEALIKHIVDKISAIRKEI 71
QY 57 REEGDE-----ETTNDVPHIQCGDGPQGLRDNSQFCLQRHQGLIFYEKLLG-- 105
DQ 72 CEKNDECENSKETLAENKLPKMEEDKGFQSGF--NOAICLIKTAGLLEYQIYDLFL 129
QY 106 SDIFGTFSLPDPSPAQLHASLLGLSLLQ-----PEGHWHETQIPLSPSPQW 156
DQ 130 QNEFEGN-----QETVMELOSSINTLIQILKEIAGLITTPATH---TDMLEKMOSSNEW 181
QY 157 QRLRLFRKILRSQAFVAAR 178
DQ 182 VKNAKVVIILRSLENFLQFSLR 203

RESULT 4
CSF3_SHEEP
ID CSF3_SHEEP STANDARD; PRT; 174 AA.
AC Q28746;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN CSF3.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP MEDLINE=95102116; PubMed=7528579;
RX O'Brien P.M., Scow H.F., Rothel J.S., Wood P.R.;
RT "Cloning and sequencing of an ovine granulocyte colony-stimulating
RT factor cDNA.";
RL DNA Seq. 4:339-342(1994).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CC CSF INDUCES GRANULOCYTES (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.

DR EMBL; X62501; CAA44363.1; -.
DR EMBL; X68723; CAA48662.1; -.
DR EMBL; A19159; CAA01443.1; -.
DR PIR; S29549; S29549.
DR HSP; P05231; IL16.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 I -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 9.0%; Score 90.5; DB 1; Length 174;
Best Local Similarity 25.5%; Pred. No. 0.12;
Matches 40; Conservative 20; Mismatches 64; Indels 33; Gaps 8;

QY 35 QLSQKCLTLANSAHP-----LVCHMDLREEGDEETNDVPHIQCGDGPQGLRDNSQFCL 90
DQ 30 ELQERLCATKHCHEPELVILGH-----SLGIPQAPL-SSCSSQSGLQTS--CL 75
QY 91 QRHOGGLIFYEKLGLSDIFTG-EPSLLPDSVAQLHASLLGLSLLQLOPGEHWHETQIIPS 149
DQ 76 DQLHGGFLYQGLL--QALAGISPELAPTLDTLQLDVDTFATNINLQME----DLGVAPA 129
QY 150 LSPSQ-----PWQRLRLFRKILRSQAFVAAR 178
DQ 130 VQPTQGTMTPTTSFAFORRAGGVLVASQLQRFGLGLAYR 166

RESULT 5
CSF3_CANFA
ID CSF3_CANFA STANDARD; PRT; 175 AA.
AC P35834;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor (G-CSF).
GN CSF3.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg D.;
RT "Crystal structure of canine and bovine granulocyte-colony
RT stimulating factor (G-CSF).";
RL J. Mol. Biol. 234:640-653(1993).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CC CSF INDUCES GRANULOCYTES.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC PDB; 1BGD; 31-OCT-93.
DR
```



RA Nagata S., Tsuchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N.,  
RA Oheda M., Nomura H., Yamazaki T.;  
RT "The chromosomal gene structure and two mRNAs for human granulocyte  
RT colony-stimulating factor.";  
RL EMBO J. 5:575-581(1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87196936; PubMed=3494801;  
RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A.,  
RA Warren M.K.;  
RT "Expression of granulocyte colony-stimulating factor by human cell  
RT lines.";  
RL J. Leukoc. Biol. 41:302-306(1987).  
RN [4]  
RP SEQUENCE FROM N.A., AND VARIANTS MET-157 AND THR-174.  
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE OF 19-207 FROM N.A.  
RX MEDLINE=86151684; PubMed=2420009;  
RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,  
RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,  
RA Barandt J., Platzer E., Moore M.A.S., Mertelsmann R., Welte K.;  
RT "Recombinant human granulocyte colony-stimulating factor: effects on  
RT normal and leukemic myeloid cells.";  
RL Science 232:61-66(1986).  
RN [6]  
RP CARBOHYDRATE-LINKAGE SITE.  
RX MEDLINE=93293942; PubMed=7685769;  
RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;  
RT "Glycosidase digestion, electrophoresis and chromatographic analysis  
RT of recombinant human granulocyte colony-stimulating factor glycoforms  
RT produced in Chinese hamster ovary cells.";  
RL J. Chromatogr. A 637:55-62(1993).  
RN [7]  
RP STRUCTURE BY NMR.  
RX MEDLINE=93106200; PubMed=1281794;  
RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;  
RT "Secondary structure of human granulocyte colony-stimulating factor  
RT derived from NMR spectroscopy.";  
RL FEBS Lett. 314:435-439(1992).  
RN [8]  
RP STRUCTURE BY NMR.  
RX MEDLINE=94304859; PubMed=7518249;  
RA Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.;  
RT "Structure and dynamics of the human granulocyte colony-stimulating  
RT factor determined by NMR spectroscopy. Loop mobility in a four-helix-  
RT bundle protein.";  
RL Biochemistry 33:8453-8463(1994).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=93281718; PubMed=7685117;  
RA Hill C.P., Oslund T.D., Eisenberg D.;  
RT "The structure of granulocyte-colony-stimulating factor and its  
RT relationship to other growth factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171(1993).  
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE  
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,  
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS  
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS  
CC CSF INDUCES GRANULOCYTES.  
CC -!- SUBUNIT: MONOMER.  
CC -!- SUBCELLULAR LOCATION: secreted.  
CC -!- PTM: O-GLYCAN CONSISTS OF GAL-GALNAC DISACCHARIDE WHICH CAN BE  
CC MODIFIED WITH UP TO TWO SIALIC ACID RESIDUES (DONE IN  
CC RECOMBINANTLY EXPRESSED G-CSF FROM CHO CELLS).  
CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine  
CC (Amgen/Roche) and Granocyte (Rhône-Poulenc). Used to treat  
CC neutropenia (a disorder characterized by an extremely low number  
CC of neutrophils in blood).  
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.  
CC -!- CAUTION: REF.4 MISQUOTES THE GENE NAME AS "CSF1".

CC -!- DATABASE: NAME-Neupogen/Granulokine;  
CC NOTE-Clinical information on Neupogen/Granulokine:  
CC WWW="http://www.neupogen.ch/monograph/frame0.htm".  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL: X03438; CAA27168.1; -  
DR EMBL: M13008; AAA03056.1; -  
DR EMBL: X03656; CAA27291.1; -  
DR EMBL: X03655; CAA27290.1; -  
DR EMBL: AF388025; AAK62469.1; -  
DR EMBL: M17706; AAA35882.1; -  
DR PIR: A24573; A24573.  
DR PIR: A25093; A25093.  
DR PDB: 1RHG; 3I-JAN-94.  
DR PDB: 1GNC; 3I-JUL-94.  
DR Genew: HGNC:2438; CSF3.  
DR MIM: 138970; -  
DR InterPro: IPR003629; GCSF\_MGF.  
DR InterPro: IPR003573; IL6\_MGF\_GCSF.  
DR Pfam: PF00489; IL6; 1.  
DR PRINTS: PR00433; IL6GCSFMGF.  
DR PRODom: PD008388; GCSF\_MGF; 1.  
DR SMART: SM00126; IL6; 1.  
DR PROSITE: PS00254; INTERLEUKIN\_6; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal; Alternative splicing;  
KW Polymorphism; Pharmaceutical; 3D-structure.  
FT SIGNAL 1 30  
FT CHAIN 31 207 GRANULOCYTE COLONY-STIMULATING FACTOR.  
FT DISULFID 69 75  
FT DISULFID 97 107  
FT CARBOHYD 166 166 O-LINKED (GALNAC. .) (BY SIMILARITY).  
FT VARSPLIC 66 68 MISSING (IN SHORT ISOFORM).  
FT VARIANT 157 157 L->M.  
FT VARIANT 174 174 /FTID=VAR\_013073.  
FT VARIANT 174 174 A->T.  
FT VARIANT 174 174 /FTID=VAR\_013074.  
FT HELIX 41 65  
FT HELIX 69 71  
FT HELIX 77 86  
FT TURN 87 88  
FT HELIX 105 124  
FT TURN 125 127  
FT TURN 130 132  
FT HELIX 133 156  
FT TURN 157 158  
FT HELIX 176 203  
FT TURN 204 204  
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;  
Query Match 8.8%; Score 88.5; DB 1; Length 207;  
Best Local Similarity 25.5%; Pred No. 0.23; 76; Indels 53; Gaps 12;  
Matches 51; Conservative 20; Mismatches 20;  
QY 15 WTAQGRAVGGSSPAWTO-----CQQ-----LSQKL---CTLAWSAHP-----LV 51  
Db ||| ||| : | : | : ||| | : | : | :  
DQ 25 WTVC-EATPLGPASSLPQSFLKCLEQVRKIQGDGAALQEKLVSECATYKLCHPPELVLL 83  
QY 52 GHMDLREDEGTNDVPHICGGCDPQGLRNSQFQRIHQGLIFEYKLLGSDFTG 111  
Db ||| ||| : | : | : ||| | : | : | :  
QY 84 GH-----SLGIPWAPL-SCFSPQALQ--LACLSQLSHGLFLQGLL--QALEG 127  
QY 112 -EPLSLPSPVAQLHASLLGLSQLQPEGHWHWETQQTIPSLSPSQ-----PWORLLLR 162  
Db ||| ||| : | : | : ||| | : | : | :  
DQ 128 ISPELGPITLDTLQLDVADFATTIQQME---ELGMAPALQPTQGAFAFAFORRAGG 183  
QY 163 FKILRSLQAFVAVAAVFAH 182



```

RN [7].
RX MEDLINE=89329059; PubMed=3262059;
RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid
RL sequence and relation to human interleukin-6."
RL Eur. J. Biochem. 176:187-197(1988).
RN [8]
RP SEQUENCE OF 66-75; 78-84 AND 128-148.
RX MEDLINE=90147691; PubMed=2302197;
RA Jahnke W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
RT "Internal amino acid sequencing of proteins by in situ cyanogen
RL bromide cleavage in polyacrylamide gels."
RL Biochem. Biophys. Res. Commun. 166:139-145(1990).
RN [9]
RP SEQUENCE OF 25-45.
RX MEDLINE=87092311; PubMed=2948184;
RA van Snick J., Cayphas S., Vink A., Uyttenhove C., Coulie P.G.,
RA Rubira M.R., Simpson R.J.;
RT "Purification and NH2-terminal amino acid sequence of a
RL T-cell-derived lymphokine with growth factor activity for B-cell
RL hybridomas."
RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X06203; CAA29560.1; -
CC DR EMBL; M20572; AAA39302.1; -
CC DR EMBL; X51457; CAA35824.1; -
CC DR EMBL; J03783; AAA39301.1; -
CC DR EMBL; X54542; CAA38411.1; -
CC DR EMBL; M24221; AAA68814.1; -
CC DR PIR; A30531; ICM56.
CC DR HSSP; P05231; 1ALU.
CC DR MGD; MGI:965559; IL6.
CC DR InterPro; IPR003573; IL6_MGF_GCSF.
CC DR InterPro; IPR003574; Interleukin_6.
CC DR Pfam; PF00489; IL6_1.
CC DR PRINTS; PR00433; IL6GCSFMGF.
CC DR ProDom; PD004356; Interleukin_6; 1.
CC DR SMART; SM00126; IL6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC DR Cytokine; Growth factor; Glycoprotein; Signal.
CC FT SIGNAL 1 24
CC FT CHAIN 25 211 INTERLEUKIN-6.
CC FT DISULFID 70 76 BY SIMILARITY.
CC FT DISULFID 99 109 BY SIMILARITY.
CC SEQUENCE 211 AA; 24384 MW; BBB47DDA9E866787A CRC64;
Query Match 8.5%; Score 85; DB 1; Length 211;
Best local similarity 22.9%; Pred. No. 0.51;
Matches 44; Conservative 20; Mismatches 58; Indels 70; Gaps 9;
QY 28 PAWTQC-----OLSKICTLAWSAHLVGHMDLREGEDEETND--VPHIQ 72
DB 44 PYVITSQVGLLTHVLWEIVEMRKELCN-----GNSDCMNDALAEKNLKPETQ 94
QY 73 CDGCDPQGLRNSQFCLQRHOGILFYE-----KLLGSD-----I 108
DB 95 RNDGCGYQGY--NQEICLLKISSGLLEYHSYLEYMKNNLKDNNKDKARVLRQDRTLIHI 152

```

```

QY 109 FTGERSLPLDSPAQLHASLL--GLSQLQPEGHWHWETQIPLSPSQPWQRLLLRKIL 166
DB 153 FNOE-----VKDLHKVILVPTPTISNALLTD-----KLESOKELWRTKTIQFIL 194
QY 167 RSLQAFVAVAAR 178
DB 195 KSLERFLKVTLR 206

RESULT 10
CSF3_BOVIN
ID CSF3_BOVIN STANDARD; PRT; 195 AA.
AC P35833; Q9TV89;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Granulocyte colony-stimulating factor precursor (G-CSF).
GN CSF3 OR GCSF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Holstein;
RA Heidari M., Kehrli M.E. Jr.;
RT "Cloning, sequencing, and analysis of cDNA encoding bovine granulocyte
RT colony stimulating factor."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94076341; PubMed=7504736;
RA Lovejoy B., Cascio D., Eisenberg D.;
RT "Crystal structure of canine and bovine granulocyte-colony
RT stimulating factor (G-CSF).";
RL J. Mol. Biol. 234:640-653(1993).
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE
CC CYTOKINES THAT ACT IN HEMATOPOIESIS BY CONTROLLING THE PRODUCTION,
CC DIFFERENTIATION AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS,
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS
CC CSF INDUCES GRANULOCYTES.
CC -!- SUBUNIT: MONOMER.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: O-GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collabora-
CC tion between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF092533; AAD16102.1; -
CC DR PDB; 1BGC; 31-OCT-93.
CC DR InterPro; IPR003629; GCSF_MGF.
CC DR InterPro; IPR003573; IL6_MGF_GCSF.
CC DR Pfam; PF00489; IL6; 1.
CC DR PRINTS; PR00433; IL6GCSFMGF.
CC DR ProDom; PD008388; GCSF_MGF; 1.
CC DR SMART; SM00126; IL6; 1.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC DR Cytokine; Growth factor; Glycoprotein; Signal; 3D-structure.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 22 195 GRANULOCYTE COLONY-STIMULATING FACTOR.
CC FT DISULFID 57 63
CC FT DISULFID 85 95
CC FT CARBOHYD 154 154
CC FT CONFLICT 93 94
CC FT HELIX 32 60

```

```

FT HELIX      65      71
FT TURN      70      75
FT HELIX      72      76
FT TURN      76      83
FT HELIX      83      89
FT TURN      87      92
FT HELIX      92     112
FT TURN     113     115
FT TURN     118     120
FT HELIX     121     145
FT HELIX     164     191
FT TURN     192
SQ SEQUENCE 195 AA; 21431 MW; 8C06119E4ADFBA73 CRC64;

Query Match      8.0%; Score 80.5; DB 1; Length 195;
Best Local Similarity 23.4%; Pred. No. 1.2;
Matches 48; Conservative 25; Mismatches 79; Indels 53; Gaps 11;

QY 7 VMLLLLLPWTAAQ-----GRAVPGSGSPAWTQ-----C-----QQLSQKLCTLAWS 46
DB 3 LMLVQLLWHSALMTVHEATPLGPARSLPQSFLLKLCLEQVRKIQADGAELQERLCAAHKL 62
QY 47 AHP-----LVGHMDLREGEDETTNDVPHIQCGDCGDPQLGNDNSQFCLQRIHOGILFIYEK 102
DB 63 CHPELMLLRH-----SLGIPQAPL-SSCSQSLSQLTS--CLNQLHGLGLFLYQG 108
QY 103 LIGSDIFTG-FPSLLPDSFVAQLHASLLGLSLLQLQPEGHWHWETOQIPSLSPSQ----- 154
DB 109 LL-QALAGISPELAPTLDTLQLOLDTFATNWLQME-----DLGAAPAVQPTQGMATFTT 162
QY 155 -PWQRLLLRFKILRSQAFVAVAR 178
DB 163 SAFQRAGGVLVASQLHRELEAYR 187

RESULT 11
ID FRZ3_DROME STANDARD; PRT; 581 AA.
AC Q77438; Q91727; Q9NTU0; Q9U902; Q9W5D5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Frizzled protein 3 precursor (Frizzled-3) (DFz3).
GN DF3 OR EG:34F3.6 OR CG16785.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=99429803; PubMed=10498678;
Sato A., Koilma T., Ui-Tei K., Miyata Y., Saigo K.;
RT "Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
of Wntless signaling in wingless hypomorphic mutants.";
RL Development 126:4421-4430(1999).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=20171076; PubMed=10704878;
Sivasankaran R., Calleja M., Morata G., Basler K.;
RT "The wingless target gene dfz3 encodes a new member of the Drosophila
Frizzled family.";
RL Mech. Dev. 91:427-431(2000).
RN [3]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D., Cadieu E.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Borkova D.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papaioannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
```

```

RA Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Sallies C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL Science 287:2220-2222(2000).
RN [4]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RX STRAIN=Berkelley; PubMed=10731132;
MEDLINE=20196006;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibagwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Morkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [5]
RP FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors
leads to the activation of the beta-catenin canonical signaling pathway, which
leads to the activation of dishevelled proteins, inhibition of
GSK-3 kinase, nuclear accumulation of beta-catenin and activation
of Wnt target genes. A second signaling pathway involving PKC and
calcium fluxes has been seen for some family members, but it is
not yet clear if it represents a distinct pathway or if it can be
integrated in the canonical pathway, as PKC seems to be required
for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem
to involve interactions with G-proteins. Required to coordinate
the cytoskeletons of epidermal cells to produce a parallel array
of cuticular hairs and bristles.
RN [6]
RP SUBCELLULAR LOCATION: Integral membrane protein (Potential).
RN [7]
RP ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
short form: are produced by alternative splicing.
RN [8]
RP TISSUE SPECIFICITY: Wing, leg and eye imaginal disks. In embryos,
expressed in seen in brain, proventriculus, Malpighian tubules,
anal plate and visceral mesoderm of parasegment 8.
RN [9]
RP DEVELOPMENTAL STAGE: Expressed in embryos from stage 11 and in
larvae.
RN [10]
RP DOMAIN: The fz domain is involved in binding with Wnt ligands (By
similarity).
RN [11]
RP SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
RECEPTORS.
```









OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Seidin M.F., Apté S.S.;  
RT "A novel gene of the ADAMTS family predicts ADAMTS-10, a  
RT metalloprotease with unique structural features and expression  
RT pattern.";  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular  
CC matrix (By similarity).  
CC -!- DOMAIN: THE SPACER DOMAIN AND THE TSP TYPE-1 DOMAINS ARE IMPORTANT  
CC FOR A TIGHT INTERACTION WITH THE EXTRACELLULAR MATRIX (By  
CC similarity).  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.  
CC -!- SIMILARITY: CONTAINS AT LEAST 4 TSP TYPE-1 DOMAINS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF302012; AAK97226.1; -  
DR InterPro; IPR000884; TSP1.  
DR SMART; SM00209; TSP1; 4.  
DR PROSITE; PS50092; TSP1; 1.  
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Repeat;  
KW Extracellular matrix.  
FT NON\_TER 1 1  
FT DOMAIN <1 51 CYS-RICH.  
FT DOMAIN 52 174 SPACER.  
FT DOMAIN 171 232 TSP TYPE-1 1.  
FT DOMAIN 234 290 TSP TYPE-1 2.  
FT DOMAIN 294 348 TSP TYPE-1 3.  
FT DOMAIN 353 399 TSP TYPE-1 4.  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 450 AA; 48861 MW; 2377D0E2CFBFBFCA CRC64;

Query Match 7.8%; Score 78.5; DB 1; Length 450;  
Best Local Similarity 24.2%; Pred. No. 5;  
Matches 36; Conservative 13; Mismatches 69; Indels 31; Gaps 6;  
QY 14 PWTAGRAVPGSSPAWTCQQLSKLCTLAWSAHLPLVGHMDLREEGDEETNDVP--- 69  
DB 179 PWTKCSAQCGSQVQVVECR---NQLDSSAVAPHYCSGSHKLPKQRACNTEPCPDWV 235  
QY 70 ---HTQCGDGDPOGLRDNQSFQRIHQGLIFYEKLGLSDIFTGEPSSLPDSPVAQLHA 126  
DB 236 VGNWRCRSCD-AGVRSRVVQRRVS-----AAEEKALDDSDACPOPRP 279  
QY 127 SLGLSQ--LIQPEGHWHWTQIPLSPS 153  
DB 280 PVLEACQGFMCPE---WATLDWSECTPS 305

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:20 ; Search time 26.0182 Seconds  
(without alignments)  
1496.757 Million cell updates/sec

Title: US-09-658-699-2

Perfect score: 1004

Sequence: 1 MLGSRAYMLLLLPWTAQR.....QAFVAARVFAGGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1004	100.0	189	4 Q9H2A5	Q9H2A5 homo sapien
2	1000	99.6	189	4 Q9NPF7	Q9NPF7 homo sapien
3	846	84.3	193	6 Q9N2H9	Q9N2H9 sus scrofa
4	784.5	78.1	196	11 Q91Z84	Q91Z84 rattus norv
5	718.5	71.6	196	11 Q9EQ14	Q9EQ14 mus musculus
6	97	9.7	195	6 Q9GJU0	Q9GJU0 felis silve
7	86	8.6	1121	16 Q9PG80	Q9PG80 xylella fas
8	85.5	8.5	352	15 Q9PZ44	Q9PZ44 multiple sc
9	84.5	8.4	363	4 Q9NRZ4	Q9NRZ4 homo sapien
10	84.5	8.4	210	11 Q9WVQ8	Q9WVQ8 mesocricetu
11	83	8.3	137	15 Q9PZ45	Q9PZ45 multiple sc
12	82	8.2	208	6 Q9XT80	Q9XT80 delphinapte
13	82	8.2	858	11 Q9Z3K0	Q9Z3K0 mus musculus
14	81.5	8.1	212	11 Q91ZL3	Q91ZL3 sigmodon hi
15	81.5	8.1	540	6 Q9SK25	Q9SK25 macaca fasc
16	80.5	8.0	232	16 O06567	O06567 mycobacteri

17	80.5	8.0	530	10 Q9C9S0	Q9C9S0 arabidopsis
18	80	8.0	215	11 Q91ZK6	Q91ZK6 sigmodon hi
19	80	8.0	324	13 Q90255	Q90255 scophthalmu
20	80	8.0	506	16 Q82LX8	Q82LX8 salmonella
21	80	8.0	633	13 Q90256	Q90256 scophthalmu
22	80	8.0	858	11 Q925D9	Q925D9 mus musculus
23	80	8.0	858	11 Q925D8	Q925D8 mus musculus
24	80	8.0	858	11 Q925A4	Q925A4 mus musculus
25	80	8.0	858	11 Q91VA4	Q91VA4 mus musculus
26	80	8.0	922	4 Q9HCG7	Q9HCG7 homo sapien
27	80	8.0	927	4 Q96SU2	Q96SU2 homo sapien
28	80	8.0	927	4 Q96A51	Q96A51 homo sapien
29	79.5	7.9	328	13 Q9YHX3	Q9YHX3 brachydanio
30	79.5	7.9	472	10 Q9LLX3	Q9LLX3 hordeum vul
31	79.5	7.9	1135	5 Q9VJF6	Q9VJF6 drosophila
32	79	7.9	134	4 Q96NR2	Q96NR2 homo sapien
33	79	7.9	506	16 Q8Z3M0	Q8Z3M0 salmonella
34	79	7.9	786	2 P95456	P95456 pantoea cit
35	78.5	7.8	207	6 Q9MYZ7	Q9MYZ7 canis fami
36	78.5	7.8	541	4 Q96AR2	Q96AR2 homo sap
37	78.5	7.8	1317	15 Q9WHI8	Q9WHI8 walleye
38	78	7.8	379	5 Q95WF6	Q95WF6 actopora ml
39	78	7.8	457	10 Q9AUV3	Q9AUV3 oryza sativ
40	78	7.8	510	2 Q93TX3	Q93TX3 stigmatella
41	78	7.8	1026	10 Q495Z9	Q495Z9 arabidopsis
42	78	7.8	1820	4 Q9P2B6	Q9P2B6 homo sapien
43	77.5	7.7	967	10 Q80540	Q80540 arabidopsis
44	76.5	7.6	399	16 Q8YY64	Q8YY64 anabaena sp
45	76.5	7.6	881	17 Q9HMG9	Q9HMG9 halobacteri

## ALIGNMENTS

RESULT 1

Q9H2A5	ID	Q9H2A5	PRELIMINARY:	PRT:	189 AA.
AC	Q9H2A5;				
DT	01-WAR-2001 (TREMBLrel. 16, Created)				
DT	01-WAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	Interleukin 23 p19 subunit.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20567322; PubMed=11114383;				
RA	Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,				
RA	Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,				
RA	Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,				
RA	Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,				
RA	Kastelein R.A.;				
RT	"Novel p19 protein Engages IL-12p40 to Form a Cytokine, IL-23, with				
RT	Biological Activities Similar as Well as Distinct from IL-12.";				
RL	Immunity 13:715-725(2000).				
DR	EMBL; AF301620; AAG37232.1; -				
DR	InterPro; IPR003573; IL6_MGF_GCSF.				
DR	SMART; SM00126; IL6; 1.				
SQ	SEQUENCE 189 AA: 20744 MW; BFB5C0F42D4C1E3A CRC64;				

Query Match	100.0%	Score 1004;	DB 4;	Length 189;
Best Local Similarity	100.0%;	Pred. No. 7.2e-96;		
Matches 189;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLGSRAYMLLLLPWTAQRAVPGGSSPAWTCQQLSQKLTCTLAWSAHPVLVGHMDLREEG	60	





Db	8	WDQCQTDLTRKKRFFFCSTAMPQYPLQGRWTWLPREGSYNYIIQLDLFCRKEGKWSFV	67		
QY	69	PHIQCGDGCDDQGLRNSQFCQLRIHQGLIFYEKLLGSDIFTGEPSLLP-----DSPVAQ	123		
Db	68	PYVQTF-----FSLRNSQLC-----KKCGL-CPTGSPQSPPPYPSVSPSPS	109		
QY	124	LHASLLGLSLLQPE-----GHHWETQQIPSLSPSQ	154		
Db	110	STNKRDPPLTQVQKEIDKGVNNEPKSANIPRLCPLQ	145		
RESULT 9					
Q9NRZ4	PRELIMINARY; PRT; 363 AA.				
ID	Q9NRZ4				
AC	Q9NRZ4;				
DT	01-OCT-2000 (TReMBLrel. 15, Created)				
DT	01-OCT-2000 (TReMBLrel. 15, Last sequence update)				
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)				
DE	Gag.				
GN	GAG.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
FN	[1]				
RP	SEQUENCE FROM N.A.				
RE	MEDLINE=20284713; PubMed=10826480;				
RX	Varisset C., Bouton O., Bedin F., Duret L., Mandrand B., Mallet F.,				
RA	Paranhos-Baccala G.;				
RA	"Chromosomal distribution and coding capacity of the human endogenous				
RT	retrovirus HERV-W family.";				
RT	AIDS Res. Hum. Retroviruses 16:731-740(2000).				
RL	EMBL; AF156961; AAF74213.1; .				
DR	InterPro; IPR000840; Gag_MA.				
DR	InterPro; IPR003036; Gag_P30.				
DR	Pfam; PF01140; Gag_MA; 1.				
DR	Pfam; PF02093; Gag_P30; 1.				
SQ	SEQUENCE 363 AA; 41075 MW; G65A4BDA473785AB CRC64;				
Query Match 8.5%; Score 85.5; DB 4; Length 363;					
Best Local Similarity 24.6%; Pred. No. 1.4;					
Matches 45; Conservative 13; Mismatches 50; Indels 75; Gaps					
QY	19	GRAVPGGSSPA-----WTQC--QOLSQ-----LCTLAWSAHPLVGHMDLRECGD-----61			
Db	2	GNIPPKAKTPLRCILENDQCDTQTLRKRTFFCSTAMPQYPLQGRWTWLPREGSYNYI 61			
QY	62	-----EETNDVPHICGDCDQGLRNSQFCQLRIHQGLIFYEKLLGSDIFTG 11			
Db	62	ILQLDLFCRKEGKWSFVQTF-----FSLRNSQLC-----KKCGL-CPTG 10			
QY	112	EPSLLP-----DSPVAQLHASLLGLSLLQPE-----GHHWETQQIPSL 15			
Db	104	SPOSPPYPSVPPPTPSSTNKDDP-----LTQTVQKEIDKGVNNEPKSANIPRLC 15			
QY	152	PSQ 154			
Db	154	PLQ 156			
RESULT 10					
Q9WQ08	PRELIMINARY; PRT; 210 AA.				
ID	Q9WQ08				
AC	Q9WQ08;				
DT	01-NOV-1999 (TReMBLrel. 12, Created)				
DT	01-NOV-1999 (TReMBLrel. 12, Last sequence update)				
DT	01-OCT-2001 (TReMBLrel. 18, Last annotation update)				
DE	IL-6 (Fragment).				
OS	Mesocricetus auratus (Golden hamster).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;				
OX	Mesocricetus.				
OX	NCBI_TaxID=10036;				



```

[1]
RP SEQUENCE FROM N.A.
RC STRAIN=APA; TISSUE=KIDNEY;
RA Nishida E.;
RT "APA hamsters IL-6 partial cDNA.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028635; BAA78766.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
FT NON_TER
SQ SEQUENCE 210 AA; 24060 MW; BD9319AFBB913AB3 CRC64;

Query Match      8.4%; Score 84.5; DB 11; Length 210;
Best Local Similarity 24.7%; Pred. No. 0.93;
Matches 44; Conservative 24; Mismatches 69; Indels 41; Gaps 8;

QY 28 PAWTCQQ-----LSQKLCITLAWSAHPLVGHMDLREEGE---ETINDVPH 70
DB 42 PVTTSQQVGLVTVLREIVELRKELC-----NNNP--GCM-----NDYVLLENLPLV 91
QY 71 IQCGGCDPQGLRDNQSQCLQRIHQGLIFYEKLLGSDIFTGEPSSLDPSPVAOLHASLLG 130
DB 92 IQINDGCLQGTG--NWEICLLKITSGLLDYQIYL--EFVTNNVDNKKDKARVIOSTIKT 147
QY 131 LSQLQPEGHWHWETQIQPS-----LSPSQPWORLLRFLRSLOAFVAVAA 178
DB 148 LSQIFQKQVGPDKIVTSPSTSKAILMEKLESQKQWERTKILKILAALEEFLEVIMR 205

RESULT 11
Q9P245 PRELIMINARY; PRT; 137 AA.
AC Q9P245;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DE gag polyprotein (fragment).
OS multiple sclerosis associated retrovirus element.
OC Viruses; Retroviridae.
OX NCBI_TaxID=89382;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99335590; PubMed=10405350;
RA Komurian-Pradel F., Paranhos-Baccala G., Bedin F., Ounanian-Paraz A.,
RA Sodoyer M., Ott C., Rajoharison A., Garcia E., Mallet F., Mandrand B.,
RA Perron H.;
RT "Molecular cloning and characterization of MSRV-related sequences
RT associated with retrovirus-like particles.";
RL Virology 260:1-9(1999).
DR EMBL; AF123880; AAD48374.1; -.
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 137 AA; 15662 MW; 8F43D05636CD958E CRC64;

Query Match      8.3%; Score 83; DB 15; Length 137;
Best Local Similarity 28.6%; Pred. No. 0.8;
Matches 28; Conservative 7; Mismatches 31; Indels 32; Gaps 5;

QY 19 GRAVPGGSPA-----WTQC--QQLSQ-----LCTLAWSAHPLVGHMDLREEGD----- 61
DB 2 GNVPEAKMPLERILENNQDQDTQLRKREIFFCSTAWPQYPLQGTWLPQGSINVINI 61
QY 62 -----ETTNDVPHIQCGDCDQGLRDNQSQFC 89
DB 62 ILQLDLCKRKQKQSEVPVQTF-----FSLRDNQSLC 94

RESULT 12
Q9XT80 PRELIMINARY; PRT; 208 AA.
AC Q9XT80;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Interleukin 6.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
RP SEQUENCE FROM N.A.
RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF076643; AAD42929.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match      8.2%; Score 82; DB 6; Length 208;
Best Local Similarity 23.9%; Pred. No. 1.7;
Matches 32; Conservative 23; Mismatches 59; Indels 20; Gaps 4;

QY 58 EEDEETTNDVPHIQCGDCDQGLRDNQSQCLQRIHQGLIFYEKLLG--SDIFTGEP 115
DB 77 KEALAEENLNLPMKAEKDCQSGF--NOETCLMRITTLGLEYQIYLDQNEYEGD--- 131
QY 116 LPDSPVAOLHASLLGLSLOLQPEGHWHWETQIQPS-----LSPSQPWORLLRFL 164
DB 132 --KGSIEAVQISIKALQILKQKVNPDVTPDPTTNASLMNQLNSQDMMRNKTIIL 189
QY 165 ILRLSLOAFVAVAA 178
DB 190 ILRLSLENLQFSLR 203

RESULT 13
Q923K0 PRELIMINARY; PRT; 858 AA.
AC Q923K0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Sweet taste receptor TIR3.
GN TASIR3 OR SAC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWR/J;
RA Nelson G., Hoon M.A., Chandrashekar J., Zhang Y., Ryba N.J.P.,
RA Zuker C.S.;
RT "Mammalian Sweet Taste Receptors.";
RL Cell 0:0-0(2001).
DR EMBL; AY032621; AAK51602.1; -.
DR MGD; MGI:1933547; Tasir3.
DR InterPro; IPR001828; ANF_receptor.
DR Pfam; PF00003; 7tm_3; 1.
DR Pfam; PF01094; ANF_receptor; 1.
```

DR PROSITE; PS00980; G\_PROTEIN\_RECEP\_F3\_2; UNKNOWN\_1.  
DR PROSITE; PS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.  
KW Receptor.  
SQ SEQUENCE 858 AA; 94530 MW; 686A7E524267796A CRC64;

Query Match 8.2%; Score 82; DB 11; Length 858;  
Best Local Similarity 27.4%; Pred No. 8.9;  
Matches 51; Conservative 10; Mismatches 65; Indels 60; Gaps 11;  
QY 3 GSRVAMLLLLPWTAGRAVPGGSPAWTQCQOLSKLCTLAWSAHLVGHMDLREEGDE 62  
DB 570 GEPWLSLLLL-----LCIVLGALAAALGLSVH-----HW----- 599  
QY 63 ETYNDVPHIQCGCDPQGLRDNISQFCLQRIHQGLIFYEKLKLGSDIFTGEP---SLLPDS 119  
DB 600 -----DSPVQASGG-----SQCFGLICGLGFLCLSVLL-----FPGRPASASCLAQQ 642  
QY 120 PVAQLHASILG-LSQLLPQEGHWHETQQIPSLSPSPQWQRLRLRFXILRSLOAFVAVAAR 178  
DB 643 PMA--HLPLTGCLSTFLQAAETFVESELP-LS-----WANWLCYS--LRGLWAWLVVLSA 693  
QY 179 VFAHGA 184  
DB 694 TFVEAA 699

## RESULT 14

Q912L3 PRELIMINARY; PRT; 212 AA.  
AC Q912L3;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)  
DE Interleukin 6.  
OS Sigmmodon hispidus (Hispid cotton rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmmodontinae;  
OC Sigmmodon.  
OX NCBI\_TaxID=42415;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PERIPHERAL BLOOD;  
RA Blanco J.C., Pletneva L.M., Prince G.A.;  
RT "Sigmmodon hispidus cytokines, chemokines and interferons."  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF421389; AAL18819.1; -  
DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
DR InterPro; IPR003574; Interleukin\_6.  
DR InterPro; IPR003580; Protachykinin.  
DR Pfam; PF00489; IL6; 1.  
DR ProDom; PD004356; Interleukin\_6; 1.  
DR SMART; SM00203; TK; 1.  
DR PROSITE; PS00254; INTERLEUKIN\_6; UNKNOWN\_1.  
SQ SEQUENCE 212 AA; 24406 MW; 97E1C47CED080D5D CRC64;

Query Match 8.1%; Score 81.5; DB 11; Length 212;  
Best Local Similarity 23.8%; Pred. No. 1.9;  
Matches 38; Conservative 25; Mismatches 64; Indels 33; Gaps 7;

QY 35 QLSQKLCFLANSAPLHVGHMDLREEGD--EETNDVPHIQCGCDPQGL-RDNSQFCLQ 91  
DB 65 QMSKELCN-----NNPCMTWDDALSENNDLPVIERNDCGCFOTGYDREN---CLL 112  
QY 92 RIHQGLIFYE---KLIGSDIFTGPELPSVLAQLHASLLGLSLLQLOPEGHWHETQIIP 148  
DB 113 KITSGLLDYQIYLEFLKKNVQDNK-----KERARVIONSTKALNAQILKQEVKDPGKTATP 167  
QY 149 S-----LSPSQPWQRLRLRFXILRSLOAFVAVAAR 178  
DB 143 SPTSKVLLMEKLESQKDWPRTKTIQLILKALEEFLKTIIMR 207

## RESULT 15

Q95K25 PRELIMINARY; PRT; 540 AA.  
AC Q95K25;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE Hypothetical 59.3 kDa protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RA Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,  
RT Terao K., Sugano S.;  
RT "Isolation of novel full-length cDNA clones from macaque testis cDNA  
libraries."  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB070002; BAB62947.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 540 AA; 59344 MW; A3ADF80610954982 CRC64;

Query Match 8.1%; Score 81.5; DB 6; Length 540;  
Best Local Similarity 28.3%; Pred. No. 5.8;  
Matches 36; Conservative 17; Mismatches 43; Indels 31; Gaps 6;

QY 54 MDLREEGDEETNDVPHIQCGCDPQ-GLRDN---SQFCLQRIHQGLIFYEKLKLGSDIF 109  
DB 415 VDMROEQLOGNTQVGERRAQAAGFAPQTGARPSETFARFCKSQ-----DSALGST-- 464  
QY 110 TGEPSLLPDSVPAQLHASLL-----GLSLLQLOPEGHWHETQIIPSLSP-----SQ 154  
DB 465 --DPAVEPTPSLDVLAQPLEASSPAEGLTOPLOGGTPHNEPCQLPSESPGSLSEVLAQ 522  
QY 155 PWQRLLL 161  
DB 523 PQGALAL 529

Search completed: November 20, 2002, 11:54:24  
Job time : 28.0182 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:39 : Search time 32.4 seconds  
(without alignments)  
777.295 Million cell updates/sec

Title: US-09-658-699-2

Perfect score: 1004

Sequence: 1 MLGSRVMLLLPWTQGR.....QAFVAVARVFAHGAATLSP 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

```

1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1004	100.0	189	20	AA1980
2	1004	100.0	189	20	AA1981
3	1004	100.0	189	21	AA1982
4	1004	100.0	189	22	AA1983
5	1000	99.6	189	21	AA1984
6	1000	99.6	189	21	AA1985
7	1000	99.6	189	22	AA1986
8	1000	99.6	189	22	AA1987
9	718.5	71.6	196	20	AA1988
10	718.5	71.6	196	20	AA1989

11	718.5	71.6	196	21	AA1982	Murine interleukin
12	718.5	71.6	196	22	AA1981	Murine IL-B30. Mu
13	463	46.1	102	20	AA1987	Partial pig interl
14	463	46.1	102	20	AA1980	Pig interleukin-B3
15	463	46.1	102	21	AA1983	Mature porcine int
16	107	10.7	175	21	AA15206	Granulopoietic act
17	105	10.5	175	21	AA15205	Granulopoietic act
18	103	10.3	175	21	AA15202	Granulopoietic act
19	103	10.3	175	21	AA15207	Granulopoietic act
20	102	10.2	174	21	AA14859	Human granulocyte
21	102	10.2	174	23	AA14695	Human G-CSF analog
22	102	10.2	175	21	AA14856	Granulopoietic act
23	102	10.2	307	16	AA19298	IL-3 containing fu
24	102	10.2	307	16	AA19299	IL-3 containing fu
25	102	10.2	307	16	AA19311	IL-3 containing fu
26	102	10.2	307	16	AA19312	IL-3 containing fu
27	102	10.2	307	21	AA153179	Human interleukin-
28	102	10.2	307	21	AA153180	Human interleukin-
29	102	10.2	307	21	AA153192	Human interleukin-
30	102	10.2	307	21	AA153193	Human interleukin-
31	102	10.2	307	22	AA13972	Myelopoietin (MPO)
32	102	10.2	307	22	AA13973	Myelopoietin (MPO)
33	102	10.2	307	22	AA13985	Myelopoietin (MPO)
34	102	10.2	307	22	AA13986	Myelopoietin (MPO)
35	102	10.2	307	22	AA14029	Myelopoietin (MPO)
36	102	10.2	307	22	AA14032	Myelopoietin (MPO)
37	102	10.2	307	22	AA14035	Myelopoietin (MPO)
38	102	10.2	307	22	AA14038	Myelopoietin (MPO)
39	102	10.2	307	22	AA14041	Myelopoietin (MPO)
40	102	10.2	307	22	AA14044	Myelopoietin (MPO)
41	102	10.2	307	22	AA14047	Myelopoietin (MPO)
42	102	10.2	307	22	AA14050	Myelopoietin (MPO)
43	102	10.2	307	22	AA14053	Myelopoietin (MPO)
44	102	10.2	307	22	AA14056	Myelopoietin (MPO)
45	102	10.2	307	22	AA14059	Myelopoietin (MPO)

#### ALIGNMENTS

RESULT 1

AA198783

ID AA198783 standard; Protein; 189 AA.

XX AA198783;

AC AA198783;

XX 04-NOV-1999 (first entry)

DT Human interleukin B30.

DE DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;

XX interleukin B30; DSR1; IL-B30; cytokine receptor; diagnosis;

KW inflammatory disorder; inflammatory response; innate immunity;

KW morphogenic development; immunological disorder.

OS Homo sapiens.

XX Key

XX Peptide

XX Protein

XX Location/Qualifiers

XX 1..21

XX /label= signal

XX 22..189

XX /label= IL-B30

XX WO9940195-A1.

XX PD 12-AUG-1999.

XX PF 05-FEB-1999;

XX 99WO-US02600.

XX PR 13-MAY-1998;

XX 98US-0078194.

XX PR 06-FEB-1998;

XX 98US-0073941.

XX (SCHE ) SCHERING CORP.

XX  
PI Kastelein RA, Mattson JD, McClanahan TK;  
XX  
DR WPI; 1999-527306/44.  
XX N-PSDB; AAZ08865.  
XX  
PT New receptor subunits useful in the treatment inflammatory disorders  
XX  
XX  
PS Claim 2; Page 26-27; 133pp; English.  
XX  
XX The present invention describes a composition (I) comprising DNAX  
XX cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
XX subunit I (DSRS1) protein, which together encode a new mammalian  
XX cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
XX proteins, or DSRS1 and IL-B30 proteins. (I) comprising DSRS1 and DCRS1  
XX is useful for screening for ligands (i.e. agonists/antagonists) from  
XX a library of compounds, which are useful for modulating the physiology  
XX or development of a cell or tissue culture e.g. inflammatory responses,  
XX innate immunity and/or morphogenic development. (R), antibodies and  
XX ligands are useful for treatment of conditions, especially immunological  
XX disorders, associated with conditions exhibiting abnormal expression of  
XX (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
XX and the subunits DSRS1 and DCRS1 are useful as immunogens for generating  
XX antibodies, or as antigens for binding antibodies. Nucleic acids  
XX encoding (R) are useful for identifying related DNAs and mRNAs, and  
XX variants from other individuals or species. The present sequence  
XX represents the specifically claimed human IL-B30, for use in the  
XX composition of the present invention.  
XX  
XX Sequence 189 AA;  
XX  
Query Match 100.0%; Score 1004; DB 20; Length 189;  
Best Local Similarity 100.0%; Pred. No. 3.2e-97;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60  
Db 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60  
Qy 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCQLRIHQGLIFVEKLGSDIFTGEPSSLDPSP 120  
Db 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCQLRIHQGLIFVEKLGSDIFTGEPSSLDPSP 120  
Qy 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWORLLRFLKILRSLOAFVAVARVF 180  
Db 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWORLLRFLKILRSLOAFVAVARVF 180  
Qy 181 AHGAATLSP 189  
Db 181 AHGAATLSP 189  
RESULT 2  
AAW95002  
XX ID AAW95002 standard; Protein; 189 AA.  
XX AC AAW95002;  
XX  
XX 21-MAY-1999 (first entry)  
XX  
XX Human interleukin-B30 (IL-B30) polypeptide.  
XX  
XX Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
XX inflammatory condition; drug screening; human.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT Peptide 1..21  
XX FT /note= "signal peptide"  
XX FT 22..189  
XX FT /note= "mature protein"  
XX

PN WO9905280-A1.  
XX  
PD 04-FEB-1999.  
XX  
PF 24-JUL-1998; 98WO-US15423.  
XX  
PR 25-JUL-1997; 97US-0900905.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Bazan JF;  
XX  
DR WPI; 1999-142935/12.  
XX N-PSDB; AAX17786.  
XX  
PT Newly isolated or recombinant polynucleotide encoding mammalian  
XX cytokine interleukin-B30 (IL-B30), including fragments - useful for  
XX regulating activation, development, differentiation and function of  
XX various cell types, and for diagnosing and treating conditions  
XX associated with IL-B30  
XX  
PS Claim 2; Page 8-9; 83pp; English.  
XX  
XX This represents a human cytokine interleukin-B30 (IL-B30) polypeptide.  
XX Host cells containing a vector comprising the IL-B30 nucleic acid are  
XX used for the recombinant production of the protein. The polynucleotides  
XX are useful for diagnosis of IL-B30 mediated conditions, and forensic  
XX science (e.g. to distinguish rodent from human, or as a marker to  
XX distinguish between different cells exhibiting differential expression or  
XX modification patterns). The IL-B30 (including fragments), together with  
XX antibodies that bind to IL-B30 are useful for teaching purposes. They  
XX are also used for treating conditions associated with abnormal physiology  
XX or development, including inflammatory conditions. The polypeptide  
XX cytokine should mediate cytokine synthesis and proliferation in cells.  
XX IL-B30 is useful for drug screening to identify compounds having binding  
XX affinity to IL-B30.  
XX  
XX Sequence 189 AA;  
XX  
Query Match 100.0%; Score 1004; DB 20; Length 189;  
Best Local Similarity 100.0%; Pred. No. 3.2e-97;  
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60  
Db 1 MLGSRVAVMLLLPWTAGRAVPGGSSPAWTCQQLSQKLCITLAWSAHPLVGHMDLREEG 60  
Qy 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCQLRIHQGLIFVEKLGSDIFTGEPSSLDPSP 120  
Db 61 DEETTNDVPHIQCGDGPQGLRDNDSQFCQLRIHQGLIFVEKLGSDIFTGEPSSLDPSP 120  
Qy 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWORLLRFLKILRSLOAFVAVARVF 180  
Db 121 VAQLHASLLGLSOLLQPEGHWHETQOIPSLSPSQPWORLLRFLKILRSLOAFVAVARVF 180  
Qy 181 AHGAATLSP 189  
Db 181 AHGAATLSP 189  
RESULT 3  
AAB01981  
XX ID AAB01981 standard; Protein; 189 AA.  
XX AC AAB01981;  
XX  
XX 27-SEP-2000 (first entry)  
XX  
XX Human interleukin-B30 (IL-B30).  
XX  
XX Interleukin-B30; IL-B30; human; cytokine; cellular signalling;  
XX immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
XX granulocyte colony stimulating factor; immune disorder;  
XX

inflammatory disease; autoimmune disease; antigen; antibody.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Peptide 1..21

XX FT Protein /note= "Signal peptide"

XX FT 22..189

XX FT /note= "Mature human IL-B30"

XX PN US0606284-A.

XX PD 09-MAY-2000.

XX PF 24-JUL-1998; 98US-0122443.

XX PR 25-JUL-1997; 97US-0053765.

XX PA (SCHE ) SCHERING CORP.

XX PI Bazan JF;

XX DR WPI; 2000-364420/31.

XX DR N-PSDB; AAA52577.

XX PT Novel recombinant DNA encoding cytokines especially interleukin-B30

XX PT useful as probes or primers for diagnosing immune disorders including

XX PT autoimmune or chronic inflammatory conditions -

XX PS Claim 1; Column 5-8; 32pp; English.

XX CC This sequence represents human interleukin-B30 (IL-B30). IL-B30

XX CC is a novel cytokine, exhibiting significant homology to IL-6 and

XX CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical

XX CC role in signalling between immune or other cells during an immune

XX CC response. The precise role of IL-B30 is not yet known - it is likely to

XX CC have either a stimulatory or an inhibitory effect on haematopoietic cells

XX CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.

XX CC Alternatively, it may affect vascular physiology or development, or have

XX CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and

XX CC antagonists are useful in the diagnosis and treatment of disorders

XX CC associated with abnormal expression or activity of IL-B30 e.g.,

XX CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are

XX CC useful for recombinant expression of IL-B30 in a host cell, and as a

XX CC source of probes and primers. The IL-B30 probes and primers can be used

XX CC to detect levels of IL-B30 expression in samples from patients suspected

XX CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may

XX CC also be used to identify homologous genes in other species. IL-B30

XX CC protein or its fragments are useful as antigens for raising antibodies to

XX CC various linear and conformational epitopes. Such antibodies may be used

XX CC to detect levels of IL-B30 protein in a sample.

XX SQ Sequence 189 AA;

Query Match 100.0%; Score 1004; DB 21; Length 189;

Best Local Similarity 100.0%; Pred. No. 3.2e-97;

Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGSRAVMLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREG 60

DB 1 MGSRAVMLLLPWTAGRAVPGSSPAWTCQQLSOKLCTLAWSAHLVGHMDLREG 60

QY 61 DEETNDVPHICGGCDPQGLRDNRSQFLRIHQGLLFYFKLGSDFTGTEGSLLPDSP 120

DB 61 DEETNDVPHICGGCDPQGLRDNRSQFLRIHQGLLFYFKLGSDFTGTEGSLLPDSP 120

QY 121 VAQLHASLGLSOLLQPEGHWHWETQIQIPSLSPQWRLRLFRKILRSLOAFVAAARVF 180

DB 121 VAQLHASLGLSOLLQPEGHWHWETQIQIPSLSPQWRLRLFRKILRSLOAFVAAARVF 180

QY 181 AHGAATLSP 189

DB 181 AHGAATLSP 189

# RESULT 4

AA847120  
ID AAB47120 standard; Protein; 189 AA.

XX  
AC AAB47120;

XX  
DT 04-JUN-2001 (first entry)

XX  
DE Human IL-B30.

XX  
KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
IFNgamma; Th1 response; autoimmune disease; chronic inflammation;  
memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;  
atherosclerosis; multiple sclerosis; vasculitis; spinal injury;  
delayed hypersensitivity; skin graft; transplant; cancer; tumour;  
stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;  
Castleman's disease.

XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers

XX  
FT Peptide 1..21

XX  
FT Protein /note= "Signal peptide"

XX  
FT 22..189 /note= "Mature protein"

XX  
PN WO200118051-A2.

XX  
PD 15-MAR-2001.

XX  
PF 08-SEP-2000; 2000WO-US24686.

XX  
PR 09-SEP-1999; 99US-0393090.

XX  
PR 10-NOV-1999; 99US-0164616.

XX  
(SCHE ) SCHERING CORP.

XX  
PI Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;  
Wiekowski MT, Lira SA, Narula SK;

XX  
PI WPI; 2001-244560/25.

XX  
DR N-PSDB; AAC85540.

XX  
PT Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its  
segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,  
atherosclerosis, multiple sclerosis, vasculitis and tumour -

XX  
PS Disclosure; Page 10-11: 69pp; English.

XX  
CC This sequence shows human interleukin-B30. Fragments of this protein  
may be used in the composition of the invention. The composition  
comprises a substantially pure polypeptide comprising a number of  
distinct segments of at least 7 contiguous amino acids from IL-12 p40  
and/or IL-B30, and a substantially pure polypeptide comprising a  
segment of at least 11 contiguous amino acids from IL-12 p40 and/or  
IL-B30. The composition is useful for modulating physiology or  
development of a cell or tissue in a host organism, resulting in an  
increased or decreased production of Interferon-gamma (IFNgamma), an  
enhanced Th1 response such as anti-tumour effect, adjuvant effect,  
anti-viral effect or antagonized allergic effect, and amelioration  
of an autoimmune condition or a chronic inflammatory condition.  
IL-B30 or its agonist is useful inducing the proliferation of memory  
T-cells. An agonist or antagonist of IL-B30 protein is useful for  
modulating the trafficking or activation of a leukocyte in an animal  
experiencing disease or symptoms of autoimmunity, an inflammatory  
condition, tissue specific autoimmunity, degenerative autoimmunity,  
rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple  
sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a  
transplant, spinal injury, stroke, neurodegeneration, an infectious  
disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's  
disease, postmenopausal osteoporosis or IL-6-associated diseases.

```
CC IL-12 p40/IL-B30 is useful as an immunogen for the production a
CC antisera or antibodies specific for binding.
XX
SQ Sequence 189 AA;
Query Match 100.0%; Score 1004; DB 22; Length 189;
Best Local Similarity 100.0%; Pred. No. 3.2e-97;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLGSRVAVMLLLLLPWTAGGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Db 1 MLGSRVAVMLLLLLPWTAGGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRTHOGLIFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRTHOGLIFYEKLLGSDIFTGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSLLQLOPEGHWHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAVARVF 180
Db 121 VAQLHASLLGLSLLQLOPEGHWHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAVARVF 180
Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189
RESULT 5
AAAY94966
ID AAAY94966 standard; Protein; 189 AA.
AC AAAY94966;
XX
XX 16-JUN-2000 (first entry)
XX Human secreted protein clone rk80_3 protein sequence SEQ ID NO:138.
XX Human: secreted protein; immunestimulant; immunesuppressant; virucide;
XX antibacterial; antifungal; cytostatic; antiinflammatory; dermatological;
XX antidiabetic; anidiasthmatic; antiarthritic; antirheumatic; protozoacide;
XX antithyroid; immune deficiency; severe combined immunodeficiency; SCID;
XX infection; HIV; hepatitis; malaria; autoimmune disorder; systemic lupus;
XX connective tissue disease; multiple sclerosis; erythematosis;
XX rheumatoid arthritis; autoimmune pulmonary inflammation; asthma;
XX Guillain-Barre syndrome; autoimmune thyroiditis; myasthenia gravis;
XX insulin dependent diabetes mellitus; graft-versus-host-disease;
XX autoimmune inflammatory eye disease; allergy.
XX
XX Homo sapiens.
XX WO200009552-A1.
XX
XX 24-FEB-2000.
XX
XX 13-AUG-1999; 99WO-US18298.
XX
XX 14-AUG-1998; 98US-0096622.
XX
XX 17-AUG-1998; 98US-0096815.
XX
XX 04-SEP-1998; 98US-0095229.
XX
XX 23-OCT-1998; 98US-0105368.
XX
XX 08-JAN-1999; 99US-0115234.
XX
XX 12-FEB-1999; 99US-0119931.
XX
XX 18-FEB-1999; 99US-0120575.
XX
XX 30-APR-1999; 99US-0132020.
XX
XX 11-AUG-1999; 99US-0096622.
XX
XX (GEMY ) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
XX Merberg D, Treacy M, Agostino Md, Steininger RJ, Spaulding V;
XX Wofg GG, Clark HF, Fachtel K;
XX
XX WPI; 2000-205979/18.
XX
```

```
PT New polynucleotides encoding secreted proteins, which may have e.g.
PT nutritional, chemokine, immune stimulating or suppressing,
PT hematopoiesis regulating, tissue growth, activin/inhibin
PT antiinflammatory or tumor inhibition activity
XX
XX Claim 147; Page 597; 64pp; English.
XX
XX AAA16618 to AAA16697 encode the human secreted proteins given in
XX
XX AAY94898 to AAY94980, isolated from human adult brain, adult thyroid,
XX adult retina, foetal carcinoma, adult blood, adult neural, foetal kidney,
XX adult placenta, adult testis, whole embryo, adult cartilage, kidney,
XX foetal brain, adult thymus, foetal placenta, adult uterus, adult tumour,
XX and adult bladder, cDNA libraries. The polynucleotides and proteins are
XX predicted to have biological activities which would make them suitable
XX for treating, preventing or ameliorating medical conditions in humans
XX and animals. The polynucleotides can be used as markers for tissues in
XX which the protein is preferentially expressed, as molecular weight
XX markers on Southern gels, and as chromosome markers or tags to identify
XX chromosomes or to map gene positions. The proteins can be used in the
XX treatment of immune deficiencies and disorders, such as severe combined
XX immunodeficiency (SCID), as well as viral, bacterial, fungal and other
XX infections. These infections include human immunodeficiency virus (HIV),
XX hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and
XX candidiasis. The proteins can be used to treat autoimmune disorders such
XX as connective tissue disease, multiple sclerosis, systemic lupus
XX erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,
XX Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependant
XX diabetes mellitus, myasthenia gravis, graft-versus-host-disease and
XX autoimmune inflammatory eye disease. The proteins can also be used to
XX treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent
XX probes for the human secreted proteins from the present invention.
XX
XX Sequence 189 AA;
Query Match 99.6%; Score 1000; DB 21; Length 189;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MLGSRVAVMLLLLLPWTAGGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Db 1 MLGSRVAVMLLLLLPWTAGGRAVPGSSPAWTCQQLSQKLCCTLAWSAHPVLVGHMDLREEG 60
Qy 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRTHOGLIFYEKLLGSDIFTGEPSSLDPSP 120
Db 61 DEETNDVPHIQCGDCDPOGLRNSQFCLQRTHOGLIFYEKLLGSDIFTGEPSSLDPSP 120
Qy 121 VAQLHASLLGLSLLQLOPEGHWHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAVARVF 180
Db 121 VGQLHASLLGLSLLQLOPEGHWHWETQIIPSLSPSPQWQRLRLKILRSLOAFVAVARVF 180
Qy 181 AHGAATLSP 189
Db 181 AHGAATLSP 189
RESULT 6
AAAY54606
ID AAAY54606 standard; Protein; 189 AA.
XX
XX AC AAAY54606;
XX
XX 01-FEB-2000 (first entry)
XX
XX SGRF protein sequence.
XX
XX SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;
XX immune system; haematopoietic system; therapy.
XX
XX Homo sapiens.
XX WO9954357-A1.
XX
XX 28-OCT-1999.
XX
```

```

XX PF 14-APR-1999; 99WO-JP01997.
XX PR 14-APR-1998; 98JP-0121805.
XX PR (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
XX PA Hirata Y;
XX PI
XX WPI: 2000-013230/01.
XX DR N-PSDB; AAZ37262, AAZ37263.
XX PR
XX PT Novel cytokine-like protein, with activity of supporting proliferation
XX PT of myeloid cells, useful in treating abnormality of cell proliferation
XX PT in immune and haematopoiesis systems
XX PS
XX PS Claim 1; Fig 1; 69pp; Japanese.
XX CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)
XX CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF
XX CC family. The protein can be used in drugs for treating diseases due to
XX CC abnormality of cell proliferation in the immune system and haematopoietic
XX CC system.
XX SQ Sequence 189 AA;

Query Match 99.6%; Score 1000; DB 21; Length 189;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPANTQCQQLSQKLTCTLAWSAHLVGHMDLREG 60
DB 1 MLGSRVAVMLLLPWTAGRAVPGGSSPANTQCQQLSQKLTCTLAWSAHLVGHMDLREG 60

QY 61 DEETNDVPHTQCGDGDQGLRDSNQFCQLRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120
DB 61 DEETNDVPHTQCGDGDQGLRDSNQFCQLRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120

QY 121 VAQLHASLLGLSQLLQPEGHWHWTQIPLSPSPQWQRLRLRKLRSLOAFVAVARVF 180
DB 121 VQQLHASLLGLSQLLQPEGHWHWTQIPLSPSPQWQRLRLRKLRSLOAFVAVARVF 180

QY 181 AHGAATLSP 189
DB 181 AHGAATLSP 189

RESULT 7
AAU12287
ID AAU12287 standard; Protein; 189 AA.
XX AC AAU12287;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO5798 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
XX KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
XX KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
XX KW adipocyte; A-peptide; factor VIIA; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US32678.
XX PR 01-DEC-1999; 99WO-US28301.
XX PR 01-DEC-1999; 99WO-US28634.
XX PR 02-DEC-1999; 99WO-US28551.

```

```

PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX
XX (GETH ) GENENTECH INC.
XX PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI: 2001-408281/43.
XX DR N-PSDB; AA521359.
XX PT Isolated, secretory and transmembrane PRO polypeptide used to detect
XX PT other PRO polypeptides, link bioactive molecules to cells expressing
XX PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX PT lung, breast, prostate, cervical
XX PS Claim 12; Fig 232; 813pp; English.
XX CC AAU12172-AAU12446 represent novel human secretory and transmembrane
XX CC PRO polypeptides. The PRO polypeptides are useful to detect other
XX CC PRO polypeptides, to link bioactive molecules to cells expressing
XX CC PRO polypeptides, to modulate biological activities of cells expressing
XX CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
XX CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
XX CC polypeptide expression in a cell sample to that in a control sample.
XX CC Some of the 275 sequences are also useful to stimulate the release of
XX CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
XX CC proliferation or differentiation of chondrocytes, the proliferation or
XX CC gene expression in pericyte cells, the release of proteoglycans from
XX CC cartilage, the proliferation of inner ear utricular supporting cells or
XX CC of T-lymphocytes, the release of a cytokine from peripheral blood
XX CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
XX CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
XX CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
XX CC to factor VIIA. The PRO polypeptides can be used in assays to identify
XX CC molecules involved in binding interactions. The polynucleotides encoding
XX CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
XX CC transgenic or knock out animals and can be used in gene therapy.
XX SQ Sequence 189 AA;

Query Match 99.6%; Score 1000; DB 22; Length 189;
Best Local Similarity 99.5%; Pred. No. 8.5e-97;
Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSSPANTQCQQLSQKLTCTLAWSAHLVGHMDLREG 60
DB 1 MLGSRVAVMLLLPWTAGRAVPGGSSPANTQCQQLSQKLTCTLAWSAHLVGHMDLREG 60

QY 61 DEETNDVPHTQCGDGDQGLRDSNQFCQLRIHQGLIFYEKLLGSDIFTGEPSSLDPSP 120

```

Db 61 DEETNDVPHIQGDCGDPQGLRDNSQFCLQRHOGLIIFYEKLLGSDIFTGEPSSLDPSP 120  
 QY 121 VAQLHASLLGSLQLQPEGHWHWTQIIPSLSPSQPWQRLLRFLKILRSLOAFVAAARVF 180  
 Db 121 VGQULHASLLGSLQLQPEGHWHWTQIIPSLSPSQPWQRLLRFLKILRSLOAFVAAARVF 180  
 QY 181 AHGAATLSP 189  
 Db 181 AHGAATLSP 189  
 RESULT 8  
 AAB48070  
 ID AAB48070 standard; protein; 189 AA.  
 XX  
 AC AAB48070;  
 XX  
 DT 19-MAR-2001 (first entry)  
 XX  
 DE Human extracellular signaling molecule (EXCS) (ID 2933038CD1).  
 XX  
 KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;  
 KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;  
 KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;  
 KW antiinfertility; cerebroprotective; nootropic; antiulcer; antifungal;  
 KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;  
 KW keratolytic; protozoacide; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200070049-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 19-MAY-2000; 2000WO-US13975.  
 XX  
 PR 19-MAY-1999; 99US-0134949.  
 PR 15-JUL-1999; 99US-0144270.  
 PR 30-JUL-1999; 99US-0146700.  
 PR 04-OCT-1999; 99US-0157508.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;  
 PI Azimzai Y, Lu DAM, Patterson C;  
 XX  
 DR WPI; 2001-025021/03.  
 DR N-PSDB; AAC84306.  
 XX  
 XX New human extracellular signaling nucleic acids and polypeptides useful  
 PT for diagnosing, treating and preventing infections and  
 PT gastrointestinal, neurological, reproductive, and  
 PT autoimmune/inflammatory disorders -  
 XX  
 PS Claim 1; Page 92; 114pp; English.  
 XX  
 XX The invention provides human extracellular signaling molecules (EXCS)  
 CC and polynucleotides which identify and encode EXCS. EXCS can be  
 CC expressed by standard recombinant methodology. The amino acid and nucleic  
 CC acid sequences of EXCS are useful for diagnosing, treating and  
 CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,  
 CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular  
 CC disease, stroke), reproductive (infertility, ovulatory defects,  
 CC endometriosis), autoimmune/inflammatory (actinic keratosis, acquired  
 CC immunodeficiency syndrome (AIDS), Addison's disease), and cell  
 CC proliferative disorders including cancers (of the breast, adrenal gland,  
 CC bone). They may also be used to treat fatal familial insomnia,  
 CC nutritional and metabolic diseases of the nervous system, myopathies,  
 CC mental disorders (anxiety, schizophrenia, mood), as well as infections  
 CC caused by parasites (malaria, leishmania, trypanosoma), viral  
 CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,  
 CC staphylococcus, bacillus), and fungal (aspergillus, blastomyces,

CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,  
 CC agonists, pharmaceutical compositions, and antibodies may also be used  
 CC for treating or preventing disorders associated with increased or  
 CC decreased expression or activity of EXCS. EXCS polynucleotides may also  
 CC be used to detect and quantify gene expression in biopsied tissues in  
 CC which expression of EXCS may be correlated with the disease, to determine  
 CC presence or excess expression of EXCS, to monitor regulation of EXCS  
 CC levels during therapeutic intervention, to detect the presence of  
 CC associated disorders, as targets in microarray, to generate hybridization  
 CC probes, and to detect differences in gene sequences among normal, carrier  
 CC or affected individuals. Antibodies may also be used in diagnosing  
 CC disorders, in monitoring patients being treated with EXCS agonists,  
 CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS  
 CC of the invention.  
 XX  
 SQ Sequence 189 AA;  
 XX  
 Query Match 99.6%; Score 1000; DB 22; Length 189;  
 Best Local Similarity 99.5%; Pred. No. 8.5e-97;  
 Matches 188; Conservative 0; Mismatches 1; Indels 0; Gaps  
 QY 1 MLGSRVAMLLLLPWTQAQRAVPGGSSPAWTCCQQLSQKLCCTLAWSAHPVGHMDLREEG 60  
 Db 1 MLGSRVAMLLLLPWTQAQRAVPGGSSPAWTCCQQLSQKLCCTLAWSAHPVGHMDLREEG 60  
 QY 61 DEETTNDVPHIQGDCGDPQGLRDNSQFCLQRHOGLIIFYEKLLGSDIFTGEPSSLDPSP 120  
 Db 61 DEETTNDVPHIQGDCGDPQGLRDNSQFCLQRHOGLIIFYEKLLGSDIFTGEPSSLDPSP 120  
 QY 121 VAQLHASLLGSLQLQPEGHWHWTQIIPSLSPSQPWQRLLRFLKILRSLOAFVAAARVF 180  
 Db 121 VGQULHASLLGSLQLQPEGHWHWTQIIPSLSPSQPWQRLLRFLKILRSLOAFVAAARVF 180  
 QY 181 AHGAATLSP 189  
 Db 181 AHGAATLSP 189  
 RESULT 9  
 AAY29784  
 ID AAY29784 standard; Protein; 196 AA.  
 XX  
 AC AAY29784;  
 XX  
 DT 04-NOV-1999 (first entry)  
 XX  
 DE Mouse interleukin B30.  
 XX  
 KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
 KW interleukin B30; DSR51; DCR51; IL-B30; cytokine receptor; diagnosis;  
 KW inflammatory disorder; inflammatory response; innate immunity;  
 KW morphogenic development; immunological disorder.  
 XX  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /label= signal  
 FT 22..196  
 FT /label= IL-B30  
 XX  
 PN WO9940195-A1.  
 XX  
 PD 12-AUG-1999.  
 XX  
 PF 05-FEB-1999; 99WO-US02600.  
 XX  
 PR 13-MAY-1998; 98US-0078194.  
 PR 06-FEB-1998; 98US-0073941.  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Kastelein RA, Mattson JD, McClanahan TK;



XX WPI; 1999-527306/44.  
 DR N-PSDB; AAZ08866.  
 XX  
 PT New receptor subunits useful in the treatment inflammatory disorders  
 XX  
 PS Claim 2; Page 27-28; 133pp; English.  
 XX  
 XX The present invention describes a composition (I) comprising DNAX  
 CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
 CC subunit I (DCRS1) protein, which together encode a new mammalian  
 CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
 CC proteins, or DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1  
 CC is useful for screening for ligands (i.e. agonists/antagonists) from  
 CC a library of compounds, which are useful for modulating the physiology  
 CC or development of a cell or tissue culture e.g. inflammatory responses,  
 CC innate immunity and/or morphogenic development. (R), antibodies and  
 CC ligands are useful for treatment of conditions, especially immunological  
 CC disorders, associated with conditions exhibiting abnormal expression of  
 CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
 CC and the subunits DCRS1 and DCRS1 are useful as immunogens for generating  
 CC antibodies, or as antigens for binding antibodies. Nucleic acids  
 CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
 CC variants from other individuals or species. The present sequence  
 CC represents the specifically claimed mouse IL-B30, for use in the  
 CC composition of the present invention.  
 XX  
 SQ Sequence 196 AA;  
 Query Match 71.6%; Score 718.5; DB 20; Length 196;  
 Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 MLGSRVAMLLLLPWTAGRAVPGGSSPAWTCQQLSQKCLTSAHPLVGHMD-LREE 59  
 DB 1 MLDCRAVIMLWLPWVTQGLAVPRSSPDWAQCCQLSRNLCMLAWNAHAPAGHMLLREE 60  
 QY 60 GDEETNDVPHIQCGDCDQGLRDNDSQFCLORIHQGLIFYEKLGSDFITGEPSPDPS 119  
 DB 61 EDEETKNVPRICEDGCDPQGLKDNSQFCLORIHQGLAFYKHLSDIFKGEPAALLPDS 120  
 QY 120 PVAQLHASLLGLSOLLQPEGHWHWTQOIPSLSPSPQWRLRLRFLKILRSLOAFVAVARV 179  
 DB 121 PMEQLHTSLGLSOLLQPEDPHRETQOMPSPSSSQWQORPLRLSKILRSLOAFVAVARV 180  
 QY 180 FAHGAATLS 188  
 DB 181 FAHGAATLT 189  
 RESULT 10  
 ID AAW95003 standard; Protein; 196 AA.  
 AC AAW95003;  
 XX  
 XX 21-MAY-1999 (first entry)  
 XX  
 DE Mouse interleukin-B30 (IL-B30) polypeptide.  
 XX  
 KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
 KW inflammatory condition; drug screening; mouse.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT /note= "signal peptide"  
 FT Protein 22..196  
 FT /note= "mature protein"  
 XX  
 PN W09905280-A1.  
 XX

PD 04-FEB-1999.  
 XX  
 PF 24-JUL-1998; 98WO-US15423.  
 XX  
 PR 25-JUL-1997; 97US-0900905.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 XX Bazan JF;  
 PI  
 XX WPI; 1999-142935/12.  
 DR N-PSDB; AAX17787.  
 XX  
 PT Newly isolated or recombinant polynucleotide encoding mammalian  
 CC cytokine interleukin-B30 (IL-B30), including fragments - useful for  
 CC regulating activation, development, differentiation and function of  
 CC various cell types, and for diagnosing and treating conditions  
 CC associated with IL-B30  
 XX  
 CC Claim 2; Page 9-10; 83pp; English.  
 XX  
 CC This represents a mouse cytokine interleukin-B30 (IL-B30) polypeptide.  
 CC Host cells containing a vector comprising the IL-B30 nucleic acid are  
 CC used for the recombinant production of the protein. The polynucleotides  
 CC are useful for diagnosis of IL-B30 mediated conditions, and forensic  
 CC science (e.g. to distinguish rodent from human, or as a marker to  
 CC distinguish between different cells exhibiting differential expression or  
 CC modification patterns). The IL-B30 (including fragments), together with  
 CC antibodies that bind to IL-B30 are useful for teaching purposes. They  
 CC are also used for treating conditions associated with abnormal physiology  
 CC or development, including inflammatory conditions. The polypeptide  
 CC cytokine should mediate cytokine synthesis and proliferation in cells.  
 CC IL-B30 is useful for drug screening to identify compounds having binding  
 CC affinity to IL-B30.  
 XX  
 SQ Sequence 196 AA;  
 Query Match 71.6%; Score 718.5; DB 20; Length 196;  
 Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
 QY 1 MLGSRVAMLLLLPWTAGRAVPGGSSPAWTCQQLSQKCLTSAHPLVGHMD-LREE 59  
 DB 1 MLDCRAVIMLWLPWVTQGLAVPRSSPDWAQCCQLSRNLCMLAWNAHAPAGHMLLREE 60  
 QY 60 GDEETNDVPHIQCGDCDQGLRDNDSQFCLORIHQGLIFYEKLGSDFITGEPSPDPS 119  
 DB 61 EDEETKNVPRICEDGCDPQGLKDNSQFCLORIHQGLAFYKHLSDIFKGEPAALLPDS 120  
 QY 120 PVAQLHASLLGLSOLLQPEGHWHWTQOIPSLSPSPQWRLRLRFLKILRSLOAFVAVARV 179  
 DB 121 PMEQLHTSLGLSOLLQPEDPHRETQOMPSPSSSQWQORPLRLSKILRSLOAFVAVARV 180  
 QY 180 FAHGAATLS 188  
 DB 181 FAHGAATLT 189  
 RESULT 11  
 ID AAB01982  
 XX  
 XX AAB01982 standard; Protein; 196 AA.  
 XX  
 XX AAB01982;  
 XX  
 DT 27-SEP-2000 (first entry)  
 XX  
 DE Murine interleukin-B30 (IL-B30).  
 XX  
 KW Interleukin-B30; IL-B30; murine; mouse; cytokine; cellular signalling;  
 KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
 KW granulocyte colony stimulating factor; immune disorder;  
 KW inflammatory disease; autoimmune disease; antigen; antibody.  
 XX

OS Mus sp.  
XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /note= "Signal peptide"  
FT Protein 22..196  
FT /note= "Mature murine IL-B30"  
XX  
XX US6060284-A.  
PN  
XX  
XX 09-MAY-2000.  
PD  
XX  
XX 24-JUL-1998; 98US-0122443.  
PF  
XX  
XX 25-JUL-1997; 97US-0053765.  
PR  
XX (SCHE ) SCHERING CORP.  
PA  
XX  
XX Bazan JF;  
FI  
XX  
XX WPI: 2000-364420/31.  
DR N-PSDB; AAA52578.  
DR  
XX  
XX Novel recombinant DNA encoding cytokines especially interleukin-B30  
PT useful as probes or primers for diagnosing immune disorders including  
FT autoimmune or chronic inflammatory conditions -  
XX  
XX  
PS Claim 1; Column 7-10; 32pp; English.  
XX  
XX This sequence represents murine interleukin-B30 (IL-B30). IL-B30  
CC is a novel cytokine, exhibiting significant homology to IL-6 and  
CC G-CSF (granulocyte colony stimulating factor). Cytokines play a critical  
CC role in signalling between immune or other cells during an immune  
CC response. The precise role of IL-B30 is not yet known - it is likely to  
CC have either a stimulatory or an inhibitory effect on haematopoietic cells  
CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.  
CC Alternatively, it may affect vascular physiology or development, or have  
CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and  
CC antagonists are useful in the diagnosis and treatment of disorders  
CC associated with abnormal expression or activity of IL-B30 e.g.,  
CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are  
CC useful for recombinant expression of IL-B30 in a host cell, and as a  
CC source of probes and primers. The IL-B30 probes and primers can be used  
CC to detect levels of IL-B30 expression in samples from patients suspected  
CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may  
CC also be used to identify homologous genes in other species. IL-B30  
CC protein or its fragments are useful as antigens for raising antibodies to  
CC various linear and conformational epitopes. Such antibodies may be used  
CC to detect levels of IL-B30 protein in a sample.  
XX  
SQ Sequence 196 AA;  
  
Query Match 71.6%; Score 718.5; DB 21; Length 196;  
Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
  
QY 1 MLGSRVAMLLLLPWTAGRAVPGCGSSPAWTCQOLSKQLCTLAWSAHLVGHMD-LREE 59  
DB 1 MIDCRVIMLLPWTGGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHWNLLREE 60  
QY 60 GDEETNDVPHITQCGDGPGLRDNQFCQLRIHQGLIFYEKLKLGSDIFTGPESSLPDS 119  
DB 61 EDEETKNVPRITQCEGDCDQGLKDNQFCQLRIHQGLIFYEKLKLGSDIFTGPESSLPDS 120  
QY 120 PVAQLHASLLGSLQLQPEGHWHETQITPSLSPQWQRLRLRPKILRSLOAFVAARV 179  
DB 121 PNEOLHTSLGSLQLQPEGHWHETQITPSLSPQWQRLRLRPKILRSLOAFVAARV 180  
QY 180 FAHGAATLS 188  
DB 181 FAHGAATLT 189

RESULT 12  
AAB47121  
ID AAB47121 standard; Protein; 196 AA.  
XX  
AC AAB47121;  
XX  
DT 04-JUN-2001 (first entry)  
XX  
DE Murine IL-B30.  
XX  
KW Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;  
KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;  
KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;  
KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;  
KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;  
KW Castleman's disease.  
XX  
OS Mus musculus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..21 /note= "Signal peptide"  
FT Protein 22..196 /note= "Mature protein"  
FT  
XX WO200118051-A2.  
XX  
XX 15-MAR-2001.  
PD  
XX 08-SEP-2000; 2000WO-US24686.  
PF  
XX 09-SEP-1999; 99US-0393090.  
PR 10-NOV-1999; 99US-0164616.  
XX (SCHE ) SCHERING CORP.  
XX Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;  
PI Wiekowski MT, Lira SA, Narula SK;  
XX WPI: 2001-244560/25.  
DR N-PSDB; AAC85541.  
XX Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its  
PT segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,  
PT atherosclerosis, multiple sclerosis, vasculitis and tumour -  
XX  
PS Disclosure; Page 11-12; 69pp; English.  
XX  
XX This sequence shows mouse interleukin-B30. Fragments of this protein  
CC may be used in the composition of the invention. The composition  
CC comprises a substantially pure polypeptide comprising a number of  
CC distinct segments of at least 7 contiguous amino acids from IL-12 p40  
CC and/or IL-B30, and a substantially pure polypeptide comprising a  
CC segment of at least 11 contiguous amino acids from IL-12 p40 and/or  
CC IL-B30. The composition is useful for modulating physiology or  
CC development of a cell or tissue in a host organism, resulting in an  
CC increased or decreased production of interferon-gamma (IFNgamma), an  
CC enhanced Th1 response such as anti-tumour effect, adjuvant effect,  
CC anti-viral effect or antagonized allergic effect, and amelioration  
CC of an autoimmune condition or a chronic inflammatory condition.  
CC IL-B30 or its agonist is useful inducing the proliferation of memory  
CC T-cells. An agonist or antagonist of IL-B30 protein is useful for  
CC modulating the trafficking or activation of a leukocyte in an animal  
CC experiencing science or symptoms of autoimmunity, an inflammatory  
CC condition, tissue specific autoimmunity, degenerative autoimmunity,  
CC rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple  
CC sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a  
CC transplant, spinal injury, stroke, neurodegeneration, an infectious  
CC disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's  
CC disease, postmenopausal osteoporosis or IL-6-associated diseases.  
CC IL-12 p40/IL-B30 is useful as an immunogen for the production a  
CC antisera or antibodies specific for binding.

SX Sequence 196 AA;  
Query Match 71.6%; Score 718.5; DB 22; Length 196;  
Best Local Similarity 74.6%; Pred. No. 3.2e-67;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLGSRVAVMLLLPWTAGRAVPGGSPAWTCCQQLSQKLTCLAWSAPLVGHMD-LREE 59  
DB 1 MLDCAVIMLWLLPWTQGLAVPRSSPDWAQCCQLSRNLCLAWNAPAGHMLLREE 60

QY 60 GDETTNDVPHIQCGDGDGQURDMSQFCLQRIHQGLIFYEKLGLSDITFTGEPSSLDP 119  
DB 61 EDEETKNVPRIQEDGCDPQGLKDNSQFCLQRIHQGLIFYEKLGLSDITFTGEPSSLDP 120

QY 120 PVAQLHASLGLSLLQLOPEGHNETQIPLSPSPQWQRLRLRFXILRSLOAFVAVARV 179  
DB 121 PNEQLHTSLLGLSLLQLOPEGHNETQIPLSPSPQWQRLRLRFXILRSLOAFVAVARV 180

QY 180 FAHGAATLS 188  
DB 181 FAHGAATLT 189

RESULT 13  
AAV29787  
ID AAV29787 standard; Protein; 102 AA.  
XX  
AC AAV29787;  
DT  
DT 04-NOV-1999 (first entry)  
DE Partial pig interleukin B30 protein.  
XX  
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW interleukin B30; DSR1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX  
OS Sus scrofa.  
XX WO9940195-A1.  
XX  
PD 12-AUG-1999.  
XX  
PF 05-FEB-1999; 99WO-US02600.  
XX  
PR 13-MAY-1998; 98US-0078194.  
PR 06-FEB-1998; 98US-0073941.  
XX  
PA (SCHE ) SCHERING CORP.  
PI Kastelein RA, Mattson JD, McManahan TK;  
XX WPI; 1999-527306/44.  
XX  
XX New receptor subunits useful in the treatment inflammatory disorders  
XX Disclosure; Page 29; 133pp; English.  
XX  
CC The present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit 1 (DCRS1) protein and DNAX soluble receptor  
CC subunit 1 (DSRS1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)  
CC proteins, or DSR1 and IL-B30 proteins. (I) comprising DSR1 and DCRS1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSR1 and DCRS1 are useful as immunogens for generating

CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the partial pig IL-B30, given in the present invention.  
XX  
SQ Sequence 102 AA;  
Query Match 45.1%; Score 463; DB 20; Length 102;  
Best Local Similarity 90.0%; Pred. No. 9.1e-41;  
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 89 CLQRIHQGLIFYEKLGLSDITFTGEPSSLDPSPVAQLHASLGLSLLQLOPEGHNETQI 148  
DB 2 CLQRIHQGLIFYEKLGLSDITFTGEPSSLDPSPVAQLHASLGLSLLQLOPEGHNETQI 61

QY 149 SLSPSPQWQRLRLRFXILRSLOAFVAVARVFAHGAATLS 188  
DB 62 SPSPSPQWQRLRLRFXILRSLOAFVAVARVFAHGAATLS 101

RESULT 14  
AAW95004  
ID AAW95004 standard; peptide; 102 AA.  
XX  
AC AAW95004;  
DT  
DT 21-MAY-1999 (first entry)  
DE Pig interleukin-B30 (IL-B30) polypeptide.  
XX  
KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
KW inflammatory condition; drug screening; pig.  
XX  
OS Sus scrofa.  
XX WO9905280-A1.  
XX  
PD 04-FEB-1999.  
XX  
PF 24-JUL-1998; 98WO-US15423.  
XX  
PR 25-JUL-1997; 97US-0900905.  
XX  
PA (SCHE ) SCHERING CORP.  
PI Bazan JF;  
XX WPI; 1999-142935/12.  
XX  
XX Newly isolated or recombinant polynucleotide encoding mammalian  
XX cytokine interleukin-B30 (IL-B30), including fragments - useful for  
XX regulating activation, development, differentiation and function of  
XX various cell types, and for diagnosing and treating conditions  
XX associated with IL-B30  
XX Claim 1; Page 11-12; 83pp; English.  
XX  
CC This invention relates to mammalian cytokine interleukin-B30 (IL-B30)  
CC polypeptides. Host cells containing a vector comprising the IL-B30  
CC nucleic acids are used for the recombinant production of the proteins.  
CC The polynucleotides are useful for diagnosis of IL-B30 mediated  
CC conditions, and forensic science (e.g. to distinguish rodent from human,  
CC or as a marker to distinguish between different cells exhibiting  
CC differential expression or modification patterns). The IL-B30 (including  
CC fragments), together with antibodies that bind to IL-B30 are useful for  
CC teaching purposes. They are also used for treating conditions associated  
CC with abnormal physiology or development, including inflammatory  
CC conditions. The polypeptide cytokine should mediate cytokine synthesis  
CC and proliferation in cells. IL-B30 is useful for drug screening to  
CC identify compounds having binding affinity to IL-B30. The present  
XX sequence represents a pig IL-B30.  
XX  
SQ Sequence 102 AA;

Query Match	46.1%	Score 463;	DB 20;	Length 102;
Best Local Similarity	90.0%	Pred. NO. 9.le-41;		
Matches	90;	Conservative	2;	Mismatches 8; Indels 0; Gaps 0;
QY	89	CLQRTHOGLIFVEKLLGSDIFTGPE	SLPDSPPVAQLHASLLGSLQLOPEGH	HWETQITP 148
Db	2	CLQRTHOGLVFEKLLGSDIFTGPE	SLHPDSCQLHASLLGLQLLOPEGH	HWETEQT 61
QY	149	SLSPSQPQWRLLLEKILRSLOAFVA	VAARVFAHGAATLS	188
Db	62	SLSPSQPQWRLLLEKILRSLOAFVA	VAARVFAHGAATLS	101
RESULT 15				
ID	AAB01983			
XX	AA	AAB01983 standard; Protein;	102 AA.	
XX	AC	AAB01983;		
XX	DT	27-SEP-2000 (first entry)		
XX	XX	Mature porcine interleukin-B30 (IL-B30).		
XX	DE			
XX	XX	Interleukin-B30; IL-B30; porcine; pig; cytokine; cellular signalling;		
KW	KW	immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;		
KW	KW	granulocyte colony stimulating factor; immune disorder;		
KW	KW	inflammatory disease; autoimmune disease; antigen; antibody.		
XX	XX			
OS	OS	Sus scrofa.		
XX	OS			
PN	PN	US6060284-A.		
XX	PD			
XX	PD	09-MAY-2000.		
XX	PF			
XX	PF	24-JUL-1998; 98US-0122443.		
XX	PR			
XX	PR	25-JUL-1997; 97US-0053765.		
XX	XX	(SCHE ) SCHERING CORP.		
PA	PA	Bazan JF;		
PI	PI			
XX	XX	WPI; 2000-364420/31.		
XX	DR			
XX	XX			
PPT	PPT	Novel recombinant DNA encoding cytokines especially interleukin-B30		
PPT	PPT	useful as probes or primers for diagnosing immune disorders including		
PPT	PPT	autoimmune or chronic inflammatory conditions -		
XX	XX			
XX	PS	Claim 1; Column 45-46; 32pp; English.		
XX	CC			
XX	CC	This sequence represents porcine interleukin-B30 (IL-B30). IL-B30		
CC	CC	is a novel cytokine, exhibiting significant homology to IL-6 and		
CC	CC	GCSF (granulocyte colony stimulating factor). Cytokines play a critical		
CC	CC	role in signalling between immune or other cells during an immune		
CC	CC	response. The precise role of IL-B30 is not yet known - it is likely to		
CC	CC	have either a stimulatory or an inhibitory effect on haematopoietic cells		
CC	CC	such as T-cells, B-cells, natural killer (NK) cells and macrophages.		
CC	CC	Alternatively, it may affect vascular physiology or development, or have		
CC	CC	neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and		
CC	CC	antagonists are useful in the diagnosis and treatment of disorders		
CC	CC	associated with abnormal expression or activity of IL-B30 e.g.,		
CC	CC	inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are		
CC	CC	useful for recombinant expression of IL-B30 in a host cell, and as a		
CC	CC	source of probes and primers. The IL-B30 probes and primers can be used		
CC	CC	to detect levels of IL-B30 expression in samples from patients suspected		
CC	CC	of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may		
CC	CC	also be used to identify homologous genes in other species. IL-B30		
CC	CC	protein or its fragments are useful as antigens for raising antibodies to		
CC	CC	various linear and conformational epitopes. Such antibodies may be used		
CC	CC	to detect levels of IL-B30 protein in a sample.		

	Query Match	46.1%	Score 463	DB 21	Length 102
	Best Local Similarity	90.0%	Pred. No. 9,1e-41		
	Matches 90	Conservative	Mismatches 8	Indels 0	Gaps
QY	89	CLQRHQGLPIFEYKLLGSDIFTGPELLDPSVAQHLASLGLSOLLQPLQPGHHWETQIP	148		
DB	2	CLQRHQGLVEYFKLLGSDIFTGPELLDPSVGVLGASLGLROLLQPLQPGHHWETQTP	61		
QY	149	SLSPSQPQWRLLLFKILRSLOAFVAAARVFAHGAATLS	188		
DB	62	SPSPSQPQWRLLLFKILRSLOAFVAAARVFAHGAATLS	101		

Search completed: November 20, 2002, 11:52:59  
Job time : 33.4 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:54:30 ; Search time 7.36364 Seconds  
(without alignments)  
401.978 Million cell updates/sec

Title: US-09-658-699-2  
Perfect score: 1004  
Sequence: 1 MLGSRVALLLLPWTQAQR.....QAFVAVARFAGHAATLSP 189

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues  
Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications.AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	101	10.1	175	10	US-09-754-532-80	Sequence 80, Appl
2	101	10.1	175	10	US-09-754-532-87	Sequence 87, Appl
3	101	10.1	175	10	US-09-754-532-88	Sequence 88, Appl
4	101	10.1	175	10	US-09-754-532-97	Sequence 97, Appl
5	100	10.0	175	10	US-09-754-532-79	Sequence 79, Appl
6	99	9.9	175	10	US-09-754-532-106	Sequence 106, App
7	98	9.8	175	10	US-09-754-532-90	Sequence 90, Appl
8	97	9.7	175	10	US-09-754-532-89	Sequence 89, Appl
9	97	9.7	175	10	US-09-754-532-110	Sequence 110, App
10	96	9.6	174	10	US-09-760-008A-1	Sequence 1, Appli
11	96	9.6	174	10	US-09-950-473-2	Sequence 2, Appli
12	96	9.6	174	12	US-10-016-403-1	Sequence 1, Appli
13	96	9.6	174	12	US-10-016-403-2	Sequence 2, Appli
14	96	9.6	174	12	US-10-003-496-1	Sequence 1, Appli
15	96	9.6	175	10	US-09-754-532-2	Sequence 2, Appli
16	96	9.6	175	10	US-09-754-532-68	Sequence 68, Appl
17	96	9.6	175	10	US-09-754-532-70	Sequence 70, Appl
18	96	9.6	175	10	US-09-754-532-78	Sequence 78, Appl
19	96	9.6	175	10	US-09-754-532-83	Sequence 83, Appl

20	96	9.6	175	10	US-09-754-532-85	Sequence 85, Appl
21	96	9.6	175	10	US-09-754-532-91	Sequence 91, Appl
22	96	9.6	175	10	US-09-754-532-93	Sequence 93, Appl
23	96	9.6	175	10	US-09-754-532-98	Sequence 98, Appl
24	96	9.6	175	10	US-09-754-532-99	Sequence 99, Appl
25	96	9.6	175	10	US-09-754-532-100	Sequence 100, App
26	96	9.6	175	10	US-09-754-532-107	Sequence 107, App
27	96	9.6	175	10	US-09-754-532-108	Sequence 108, App
28	96	9.6	175	10	US-09-230-733-1	Sequence 1, Appli
29	96	9.6	175	10	US-09-818-430A-2	Sequence 2, Appli
30	96	9.6	177	10	US-09-984-186-14	Sequence 14, Appl
31	96	9.6	348	12	US-10-003-496-6	Sequence 6, Appli
32	96	9.6	787	10	US-09-984-186-16	Sequence 16, Appl
33	95	9.5	175	10	US-09-754-532-67	Sequence 67, Appl
34	95	9.5	175	10	US-09-754-532-75	Sequence 75, Appl
35	95	9.5	175	10	US-09-754-532-92	Sequence 92, Appl
36	95	9.5	175	10	US-09-754-532-94	Sequence 94, Appl
37	95	9.5	175	10	US-09-754-532-105	Sequence 105, App
38	95	9.5	175	10	US-09-754-532-109	Sequence 109, App
39	93.5	9.3	174	12	US-10-016-403-3	Sequence 3, Appl
40	93.5	9.3	175	10	US-09-754-532-86	Sequence 86, Appl
41	93.5	9.3	175	10	US-09-754-532-95	Sequence 95, Appl
42	93.5	9.3	175	10	US-09-754-532-102	Sequence 102, App
43	93	9.3	175	10	US-09-754-532-69	Sequence 69, Appl
44	93	9.3	175	10	US-09-754-532-73	Sequence 73, Appl
45	93	9.3	175	10	US-09-754-532-76	Sequence 76, Appl

ALIGNMENTS

RESULT 1  
US-09-754-532-80  
; Sequence 80, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Osslund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: Amgen Center, 1840 Dehavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/754,532  
; FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/448,716  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Pessin, Karol  
REGISTRATION NUMBER: 34,899  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 805/499-5725  
TELEFAX: 805/499-8011  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 175 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-754-532-80

Query Match 10.1%; Score 101; DB 10; Length 175;

```

QY 127 SLGLSOLLQPGHHWETQQIPSPSQ-----PWORLLLRFKILRSQAQFAVAAR 178
      :   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 ADFATTIWQOME---ELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEYSYR 167

QY 179 VFAH 182
      | |
Db 168 VLRH 171

RESULT 3
US-09-754-532-88
; Sequence 88, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-88

Query Match 10.1%; Score 101; DB 10; Length 175;
Best Local similarity 26.6%; Pred. No. 0.0046;
Matches 49; Conservative 19; Mismatches 76; Indels 40; Gaps

QY 12 LLPWTAQGRAVPGGSSPAWTCQQLSKLCTLAWSAHP----LVGHMDLRREGDETTND 67
      || || || | | | | | | | | | | | | | | | | | | | | | |
Db 15 LKLCIAQVRKIQGDGA-----ALQEKLCATKYLCHPEELVLLGH-----SLG 56

QY 68 VPHIQGDCDDPQGLRNSQFCIORIHQGLIFXEKLIGSDIFTG-EPSELLPDSVPAQLHA 126
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 IPWAPL-SCSPSQAQ--LAGCLISQLSHGLFYOGLL--QALEGISPELGPTLOTQLQDV 111

QY 127 SLGLSOLLQPGHHWETQQIPSPSQ-----PWORLLLRFKILRSQAQFAVAAR 178
      :   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 112 ADFATTIWQOME---ELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEYSYR 167

QY 179 VFAH 182
      | |
Db 168 VLRH 171

RESULT 4
US-09-754-532-97

```

```
; Sequence 97, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-97

Query Match 10.1%; Score 101; DB 10; Length 175;
Best Local Similarity 26.6%; Pred. No. 0.0046;
Matches 49; Conservative 19; Mismatches 76; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQLSKLCTLAWSAHP-----LVGHMDLREEGDEETND 67
Db 15 LLKLAQVRKIQDGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 56
QY 68 VPHIOGDCDQGLRDNQSFCLQRIHQGLIFYEKLKLGSDIFTG-EPSLLPDSFVAQLHA 126
Db 57 IPWAPL-SSCPQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGTLDTLQLDV 111
QY 127 SLGLSQLQPEGHWHETQIPSLSPSQ-----PWQRLLRFKILRSQAFAVAAR 178
Db 112 ADFATTIWQME---ELGMAPALQPTQGAPAFASAFORRAGGVLVASHLQSFLEVSYR 167
QY 179 VFAH 182
Db 168 VLRH 171

RESULT 5
US-09-754-532-79
; Sequence 79, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
```

```
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-754-532-79

Query Match 10.0%; Score 100; DB 10; Length 175;
Best Local Similarity 26.7%; Pred. No. 0.0058;
Matches 50; Conservative 19; Mismatches 78; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQQLSKLCTLAWSAHP-----LVGHMDLREEGDEETND 67
Db 15 LLKLEQVRKIQDGA-----ALQEKLCATYKLCHEPELVLLGH-----SLG 56
QY 68 VPHIOGDCDQGLRDNQSFCLQRIHQGLIFYEKLKLGSDIFTG-EPSLLPDSFVAQLHA 126
Db 57 IPWAPL-SSCPQALQ--LAGCLSQLHSGFLYQGLL--QALEGISPELGTLDTLQLDV 111
QY 127 SLGLSQLQPEGHWHETQIPSLSPSQ-----PWQRLLRFKILRSQAFAVAAR 178
Db 112 ADFATTIWQME---ELGMAPALQPTQGAPAFASAFORRAGGVLVASHLQSFLEVSYR 167
QY 179 VFAH 185
Db 168 VLRH 174

RESULT 6
US-09-754-532-106
; Sequence 106, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
```

```

; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-90

      Query Match          9.8%; Score 98; DB 10; Length 175;
Best Local Similarity    26.1%; Pred.No. 0.0093;
Matches 48; Conservative 20; Mismatches 76; Indels 40; Gaps 9;

QY   12 LLPWTAQGAVPGGSSPAWTCQQSLKSOKLCTPLAWSAHP-----LVGRMDLREEGEDEFTTND 67
     ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   15 LKLCSEQVKIQGDGA-----ALQEKLCAITYKLCHPEELVLIGH-----SLG 56

QY   68 VPHIQCGDCDPQGLRDNSTFCQLRIHQGLIFYEKLGLSDIFTG--BPSLLPSPVAOLHA 126
     ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   57 IPWAPL--SSCPSQLQ--LAGCLSQHSGFLYIGLL--QALEGISPELGPTLTDLTLQLDV 111

QY   127 SILGLSOLLQPGECHHWETQIPSPSPQ-----PWQRLLRFKLRSLOAFVAAVAR 178
     : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db   112 ADFATTIWOOME-----ELGEAPALQPTGAMPAPAFSAFQRRAGGVILVASHLQSFSLEVSYR 167

QY   179 VFAH 182
     | |
Db   168 VLRH 171

```

RESULT 8  
US-09-754-532-89

```

US-09-754-532-89
; Sequence 89, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Oslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754.532

```

FILING DATE:

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 175 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-09-754-532-89

Query Match          9.7%; Score 97; DB 10; Length 175;
Best Local Similarity 26.1%; Pred. No. 0.012;
Matches 48; Conservative 19; Mismatches 77; Indels

OV      12 LIPPTAGGRAVPGSSSPANTOCQOI SQKICTTAMSAHP---LVGHMDLREFGDN

```

QY 12 LLPWTAQGRAVPGGSSPAWTQCQQLSQKLCTLAWSAHP----LVGHMDLREEGDEETND 67



Db 15 LLKCLEQVRKIOGAGA-----ALQEKLCATYKLCHEPELVLLGH-----SIG 56  
QY 68 VPHIQCGDCDQGLRDNQFCQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSFVAQLHA 126  
Db 57 IPWAPL-SSCPSQALQ--LAGCLSQHSGLFLYQGLL--QALEGISPELGTDLTLDLV 111  
QY 127 SLLGLSOLLQPEGHWHWTQQIPSLPSQO-----PWQRLLLRFRKILRSLOAFVAVAR 178  
Db 112 ADFATTIWOQME-----ELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYR 167  
QY 179 VFAH 182  
Db 168 VLRH 171  
RESULT 9  
US-09-754-532-110  
; Sequence 110, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Ossiund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amgen Inc.  
; STREET: Amgen Center, 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/09754,532  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/448,716  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fesslin, Karol  
; REGISTRATION NUMBER: 34,899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/499-5725  
; TELEFAX: 805/499-8011  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-754-532-110

Query Match 9.7%; Score 97; DB 10; Length 175;  
Best Local Similarity 26.1%; Pred. No. 0.012;  
Matches 48; Conservative 20; Mismatches 76; Indels 40; Gaps 9;  
QY 12 LLPWTAAGRAVPGGSSPAWTCQQLSQKLCITLANSAP-----LVGHMDLREEGDEETND 67  
Db 15 LLKCLEQVRKIOGAGA-----ALQEKLCATYKLCHEPELVLLGH-----SIG 56  
QY 68 VPHIQCGDCDQGLRDNQFCQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSFVAQLHA 126  
Db 57 IPWAPL-SSCPSQALQ--LAGCLSQHSGLFLYQGLL--QALEGISPELGTDLTLDLV 111  
QY 127 SLLGLSOLLQPEGHWHWTQQIPSLPSQO-----PWQRLLLRFRKILRSLOAFVAVAR 178  
Db 112 ADVATTIWOQME-----ELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYR 167

QY 179 VFAH 182  
Db 168 VLRH 171  
RESULT 10  
US-09-760-008A-1  
; Sequence 1, Application US/09760008A  
; Patent No. US20020004483A1  
; GENERAL INFORMATION:  
; APPLICANT: NISSEN, TORBEN LAUESGAARD  
; APPLICANT: ANDERSEN, KIM VILBOUR  
; APPLICANT: HANSEN, CHRISTIAN KARSTEN  
; APPLICANT: MIKKELSEN, JAN MOLLER  
; TITLE OF INVENTION: G-CSF CONJUGATES  
; FILE REFERENCE: 31-000700US  
; CURRENT APPLICATION NUMBER: US/09760,008A  
; CURRENT FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: 60/176,376  
; PRIOR FILING DATE: 2000-01-14  
; PRIOR APPLICATION NUMBER: 60/189,506  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 60/215,644  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: DK PA 2000 00024  
; PRIOR FILING DATE: 2000-01-10  
; PRIOR APPLICATION NUMBER: DK PA 2000 00341  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: DK PA 2000 00943  
; PRIOR FILING DATE: 2000-06-16  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-008A-1  
Query Match 9.6%; Score 96; DB 10; Length 174;  
Best Local Similarity 26.1%; Pred. No. 0.015;  
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;  
QY 12 LLPWTAAGRAVPGGSSPAWTCQQLSQKLCITLANSAP-----LVGHMDLREEGDEETND 67  
Db 14 LLKCLEQVRKIOGAGA-----ALQEKLCATYKLCHEPELVLLGH-----SIG 55  
QY 68 VPHIQCGDCDQGLRDNQFCQRIHQGLIFYEKLLGSDIFTG-EPSLLPDSFVAQLHA 126  
Db 56 IPWAPL-SSCPSQALQ--LAGCLSQHSGLFLYQGLL--QALEGISPELGTDLTLDLV 110  
QY 127 SLLGLSOLLQPEGHWHWTQQIPSLPSQO-----PWQRLLLRFRKILRSLOAFVAVAR 178  
Db 111 ADFATTIWOQME-----ELGMAPALOPTQGAMPAPAFASAFQRRAGGVLVASHLQSFLEVSYR 166  
QY 179 VFAH 182  
Db 167 VLRH 170  
RESULT 11  
US-09-950-473-2  
; Sequence 2, Application US/09950473  
; Patent No. US20020151488A1  
; GENERAL INFORMATION:  
; APPLICANT: Sarkar, Casim  
; APPLICANT: Laufemburger, Douglas  
; TITLE OF INVENTION: G-CSF Analog Compositions and Methods  
; FILE REFERENCE: 01017/37732  
; CURRENT APPLICATION NUMBER: US/09/950,473  
; CURRENT FILING DATE: 2001-09-10  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 2



```
QY 12 LLPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHP-----LVGHMDLREGEDETTND 67
Db 14 LLKLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 55
QY 68 VPHIOCGDGDPOGLRDNQSQCLORIHQGLIFYEKLIGSDIFTG-EPSSLDPSPVAQLHA 126
Db 56 IPWAPL-SSCPSQALQ--LAGCLSQLSHGLFLYQGLL--QALEGISPELGPTLDTLQLDV 110
QY 127 SLGLSOLLQPEGHWHWTQOIPSLSPSQ-----PWQRLLRFKILRSLOAFVAVAAAR 178
Db 111 ADFATTIWQOME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 166
QY 179 VFAH 182
Db 167 VLRH 170
```

```
RESULT 14
US-10-003-496-1
; Sequence 1, Application US/10003496
; Patent No. US20020142964A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Aps
; TITLE OF INVENTION: Single-Chain Polypeptides
; FILE REFERENCE: 0218US210
; CURRENT APPLICATION NUMBER: US/10/003,496
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/245,727
; PRIOR FILING DATE: 2000-11-02
; NUMBER OF SEQ. ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-003-496-1
```

```
Query Match 9.6%; Score 96; DB 12; Length 174;
Best Local Similarity 26.1%; Pred. No. 0.015;
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHP-----LVGHMDLREGEDETTND 67
Db 14 LLKLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 55
QY 68 VPHIOCGDGDPOGLRDNQSQCLORIHQGLIFYEKLIGSDIFTG-EPSSLDPSPVAQLHA 126
Db 56 IPWAPL-SSCPSQALQ--LAGCLSQLSHGLFLYQGLL--QALEGISPELGPTLDTLQLDV 110
QY 127 SLGLSOLLQPEGHWHWTQOIPSLSPSQ-----PWQRLLRFKILRSLOAFVAVAAAR 178
Db 111 ADFATTIWQOME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 166
QY 179 VFAH 182
Db 167 VLRH 170
```

```
RESULT 15
US-09-754-532-2
; Sequence 2, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: Amgen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
```

```
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-2

Query Match 9.6%; Score 96; DB 10; Length 175;
Best Local Similarity 26.1%; Pred. No. 0.015;
Matches 48; Conservative 19; Mismatches 77; Indels 40; Gaps 9;

QY 12 LLPWTAQGRAVPGSSPAWTCQOOLSKLCTLAWSAHP-----LVGHMDLREGEDETTND 67
Db 15 LLKLEQVRKIQGDGA-----ALQEKLCATYKLCHPPELVLLGH-----SLG 56
QY 68 VPHIOCGDGDPOGLRDNQSQCLORIHQGLIFYEKLIGSDIFTG-EPSSLDPSPVAQLHA 126
Db 57 IPWAPL-SSCPSQALQ--LAGCLSQLSHGLFLYQGLL--QALEGISPELGPTLDTLQLDV 111
QY 127 SLGLSOLLQPEGHWHWTQOIPSLSPSQ-----PWQRLLRFKILRSLOAFVAVAAAR 178
Db 112 ADFATTIWQOME----ELGMAPALQPTQGAMPAPAFASAFORRAGGVLVASHLQSFLEVS 167
QY 179 VFAH 182
Db 168 VLRH 171

Search completed: November 20, 2002, 12:00:55
Job time : 8.36364 secs
```



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1004	100.0	189	3	US-09-122-443-2	Sequence 2, Appli
2	718.5	71.6	196	3	US-09-122-443-4	Sequence 4, Appli
3	463	48.1	102	3	US-09-122-443-5	Sequence 5, Appli
4	102	10.2	307	3	US-08-469-318-121	Sequence 121, App
5	102	10.2	307	3	US-08-469-318-122	Sequence 122, App
6	102	10.2	307	3	US-08-469-318-134	Sequence 134, App
7	102	10.2	307	3	US-08-469-318-135	Sequence 135, App
8	102	10.2	307	3	US-08-468-609A-121	Sequence 121, App
9	102	10.2	307	3	US-08-468-609A-122	Sequence 122, App
10	102	10.2	307	3	US-08-468-609A-134	Sequence 134, App
11	102	10.2	307	3	US-08-468-609A-135	Sequence 135, App
12	102	10.2	307	4	US-08-446-872A-121	Sequence 121, App
13	102	10.2	307	4	US-08-446-872A-122	Sequence 122, App
14	102	10.2	307	4	US-08-446-872A-134	Sequence 134, App
15	102	10.2	307	4	US-08-446-872A-135	Sequence 135, App
16	102	10.2	307	4	US-08-762-227A-121	Sequence 121, App
17	102	10.2	307	4	US-08-762-227A-122	Sequence 122, App
18	102	10.2	307	4	US-08-762-227A-134	Sequence 134, App
19	102	10.2	307	4	US-08-762-227A-135	Sequence 135, App
20	102	10.2	307	5	PCF-US95-01185-121	Sequence 121, App
21	102	10.2	307	5	PCF-US95-01185-122	Sequence 122, App
22	102	10.2	307	5	PCF-US95-01185-134	Sequence 134, App
23	102	10.2	307	5	PCF-US95-01185-135	Sequence 135, App
24	101	10.1	175	1	US-08-010-099-80	Sequence 80, Appl
25	101	10.1	175	1	US-08-010-099-87	Sequence 87, Appl
26	101	10.1	175	1	US-08-010-099-88	Sequence 88, Appl
27	101	10.1	175	1	US-08-010-099-97	Sequence 97, Appl

Qy	1	MLGSRAYMILLLLPWTQAQGRAVFCGGSPAWTQCQOILSQKCLCTLANSAHPLVGHMD-LRRE	59
Dd	1	MDCRAVIMLWLLPWVTQGLAVPRSSPDWAQQOQLSRNLCMLANAHAPAGHMNLRLRE	60
Qy	60	GDEETTDNDPHIQCGDCCDPQGLRDNSQFCLRIRHGGLIFYEKKLGSDITFTGEPSLLPDS	119
Dd	61	EDEETKNVPRIQCEDCDCCDPQGLKDNSQFCLRIRQGAFYKHLDDSIDFKGEPA LLPDS	120
Qy	120	PVAQLHASLLGSLLQPFGHHWETQIIPSLSPSQPMQRLLLRFKILRSLOAFVAARY	179
Dd	121	PMEQLHTSLLGSLLQPEDHPRETQTQMPSILSSQQWORPLLRSKLRSLOAFLAAARV	180
Qy	180	FAGHAATLS	188

```

Db      181 FAHGAATLT 189

RESULT 3
US-09-122-443-5
; Sequence 5, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122.443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-5

Query Match 46.1%; Score 463; DB 3; Length 102;
Best Local Similarity 90.0%; Pred. No. 2,1e-45;
Matches 90; Conservative 2; Mismatches 8; Indels 0; Gaps

Qy      89 CLQRHGLFYFKLLGSDIFTGEPSSLDPSPVAQLHASLLGLSOLLQPEGHHWETQIP 148
Db      2 CLQRHGLFYFKLLGSDIFTGEPSSLDPGSGVQLHASLLGLRQLLQPEGHHWETQTP 61

Qy      149 SLSPSQWQRLLRFLKRLSLQAFVAAVFAHGAATLS 188
Db      62 SPSPSQWQRLLRFLKRLSLQAFVAAVFAHGAATLS 101

RESULT 4
US-08-469-318-121
; Sequence 121, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

```



Wed Nov 20 13:28:56 2002

```

/ TITLE OF INVENTION: Protein
/ NUMBER OF SEQUENCES: 196
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/469,318
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/446,872
/ FILING DATE:
/ INFORMATION FOR SEQ ID NO: 135:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 307 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-469-318-135

```

Query Match	10.28;	Score 102;	DB 3;	Length 307;
Best Local Similarity	24.8%;	Pred. No. 0.0016;		
Matches 52;	Conservative	20;	Mismatches 76;	Indels 62; Gaps 10;
QY	15	WTAQGRAVPGSS-----PAWTQCOQ-----	LSOKLCTLAW	45
		:		
Db	114	YVTEGRISPGGGGGSNMATPLQSPFLKLSLEQVRKIQDGAALQEKLCATYK	173	
QY	46	SAHP-----LVGHMDLRREEDDEETNDVPHTIOGGDQGLRDSQFCFLORHOGLIFFE	101	
		:         :     :     :     :     :		
Db	174	LCHPEELVLVGH-----SIGTPWAPL--SCSPQALQ--LACLSQLHSGGLFLYQ	219	
QY	102	KLLGSDIFTG--EPSLLPSPVAQHASLLGLLSQLQPEGHWHWTQTTPSLSPSQ-----	154	
		:		
Db	220	GLL--QALGEGISPELCPTLTLDQVDVFTIQQWE---ELGMAPALQPTQGAPAF	273	
QY	155	--PWQRLLRFKILRSLOAFVAAARFAH	182	
		:     :         :		
Db	274	ASAFORRAGGVILVASHLQSFLEVSRYLRH	303	

```

1  RESULT 8
2  US-08-468-609A-121
3  ; Sequence 121, Application US/08468609A
4  ; Patent No. 6030812
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Abrams, Mark A.
7  ; APPLICANT: Bauer, S. C.
8  ; APPLICANT: Braford-Goldberg, Sarah
9  ; APPLICANT: Caparon, Maïre H.
10 ; APPLICANT: Easton, Alan M.
11 ; APPLICANT: Klein, Barbara K.
12 ; APPLICANT: McKearn, John P.
13 ; APPLICANT: Ollins, Peter O.
14 ; APPLICANT: Paik, Kuman
15 ; APPLICANT: Thomas, John W.
16 ; TITLE OF INVENTION: Fusion Protein
17 ; NUMBER OF SEQUENCES: 197
18 ; CORRESPONDENCE ADDRESS:
19 ; ADDRESSEE: Dennis A. Bennett, G.
20 ; ADDRESSEE: Corporate Patent Dept
21 ; STREET: P. O. Box 5110
22 ; CITY: Chicago
23 ; STATE: Illinois
24 ; COUNTRY: USA
25 ; ZIP: 60680
26 ; COMPUTER READABLE FORM:
27 ; MEDIUM TYPE: Floppy disk
28 ; COMPUTER: IBM PC compatible
29 ; OPERATING SYSTEM: PC-DOS/MS-DOS
30 ;

```

```

: APPLICANT: Thomas, John W.
: TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (II-
: NUMBER OF SEQUENCES: 197
: CORRESPONDENCE ADDRESS:
: ADDRESS: Dennis A. Bennett, G.D. Searle & Co.,
: ADDRESS: Corporate Patent Dept.
: STREET: P. O. Box 5110
: City: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60680
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
:

```

```

, SOFTWARE: PatentIn Release #1.0, Version #1.25
,
, CURRENT APPLICATION DATA:
,
, APPLICATION NUMBER: US/08/468,609A
,
, FILING DATE: 06-JUN-1995
,
, CLASSIFICATION:
,
, PRIOR APPLICATION DATA:
,
, APPLICATION NUMBER: US 08/192,325
,
, FILING DATE: 14-FEB-1994
,
, ATTORNEY/AGENT INFORMATION:
,
, NAME: Bennett, Dennis A.
,
, REGISTRATION NUMBER: 34,547
,
, REFERENCE/DOCKET NUMBER: C-2790/3
,
, TELECOMMUNICATION INFORMATION:
,
, TELEPHONE: (314)737-6986
,
, TELEFAX: (314)737-6972
,
, INFORMATION FOR SEQ ID NO: 121:
,
, SEQUENCE CHARACTERISTICS:
,
, LENGTH: 307 amino acids
,
, TYPE: amino acid
,
, STRANDEDNESS:
,
, TOPOLOGY: linear
,
, MOLECULE TYPE: protein
,
, US-08-468-609A-121

```

```

Query Match      10.28; Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 74; Mismatches 74; Indels 62; Gaps 11;

QY 15 WTAQGRAVPGSS-----PAWT-----QCQQ-----LSQKLCITLAW 45
      : :| | | | | : : : : : : : : : : : : : : :
Db 114 YVIEGRISFGSGSGGSGSNWATPLGPASSLPQSLKLEQVRKIQDGAALQKLCATYK 173
      : :| | | | | : : : : : : : : : : : : : : :

QY 46 SAHP-----IVGHMDLREGEDETTNDVPHIOGGGCDPQGLRDNQFCQRIHQGLIFYE 101
      : :| | : : : : : : : : : : : : : : : : : : :
Db 174 LCHPEELVLVIGH-----SLGIPWAPL-SCCPSQALQ--LAGLUSQLHSGFLFYQ 219
      : :| | : : : : : : : : : : : : : : : : : : :

QY 102 KLIGSDIFTG-PESLLPDPSPVAALHASLLGLSQLLQPEGHWHWTQQTPSLSPSQ----- 154
      || || : : : : : : : : : : : : : : : : : : :
Db 220 GLI--QAEGISPELQPTLDTLQLDVADFATTIQQWE---ELGMAPALQPTGGAMPAF 273
      : :| | : : : : : : : : : : : : : : : : : : :

QY 155 --PWQRLLLRFKILRSLOAFVAVARFAH 182
      : :| | : : : : : : : : : : : : : : : : : : :
Db 274 ASAFORRAGGVLVASHLOSFLFVSVRYLRH 303
      : :| | : : : : : : : : : : : : : : : : : : :

```

```

RESULT 9
US-08-468-609A-122
; Sequence 122, Application US/08468609A
; Patent No. 6030812
;
; GENERAL INFORMATION:
;   APPLICANT: Abrams, Mark A.
;   APPLICANT: Bauer, S. C.
;   APPLICANT: Braford-Goldberg, Sarah
;   APPLICANT: Caparon, Maïre H.
;   APPLICANT: Easton, Alan M.
;   APPLICANT: Klein, Barbara K.
;   APPLICANT: McKearn, John P.
;   APPLICANT: Olins, Peter O.
;   APPLICANT: Paik, Kuman
;   APPLICANT: Thomas, John W.
;
; TITLE OF INVENTION: Fusion Protein
;
; NUMBER OF SEQUENCES: 197
;
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Dennis A. Bennett, G.
;   ADDRESSEE: Corporate Patent Dept
;   STREET: P. O. Box 5110
;   CITY: Chicago
;   STATE: Illinois
;   COUNTRY: USA
;
; ZIP: 60680
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible

```



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/468,609A  
APPLICATION NUMBER: US/08/468,609A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 122:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-609A-122

Query Match 10.28; Score 102; DB 3; Length 307;  
Best Local Similarity 24.88; Pred. No. 0.0016;  
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;  
QY 15 WTAQGRVPGGSS-----PAWTQCQ-----LSOKLCTLAW 45  
DB 114 VYIEGRISPGGGSGGSMATPLGPASSLPQSFLKLEQVRKIQDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEDDEETNDVPHIQCGDQGLRDNQSFCLORIHOGLIFYE 101  
DB 174 LCHPEELVLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSQLHSGFLYQ 219  
QY 102 KLIGSDIFTG--EPSLLPDPSPAQLHASLLGSQLQPEGHWHWETQQTIPSLSPSQ----- 154  
DB 220 GLL--QALEGISPELGPFTLDTLQDLDVADFATTIWOQME----ELGMAPALQPTQGAMP 273  
QY 155 --PWORLLRKFILRSLOAFVAVAAVFAH 182  
DB 274 ASAFORRAGGVLVASHLQSFLEVSRYVLRH 303

RESULT 10  
US-08-468-609A-134  
Sequence 134, Application US/08468609A  
Patent No. 6030812  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Mair H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kumnan  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM: Floppy disk  
MEDIUM TYPE:

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/468,609A  
APPLICATION NUMBER: US/08/468,609A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 134:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-609A-134

Query Match 10.28; Score 102; DB 3; Length 307;  
Best Local Similarity 24.88; Pred. No. 0.0016;  
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;  
QY 15 WTAQGRVPGGSS-----PAWT-----CQOQ-----LSOKLCTLAW 45  
DB 114 VYIEGRISPGGGSGGSMATPLGPASSLPQSFLKLEQVRKIQDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREEDDEETNDVPHIQCGDQGLRDNQSFCLORIHOGLIFYE 101  
DB 174 LCHPEELVLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSQLHSGFLYQ 219  
QY 102 KLIGSDIFTG--EPSLLPDPSPAQLHASLLGSQLQPEGHWHWETQQTIPSLSPSQ----- 154  
DB 220 GLL--QALEGISPELGPFTLDTLQDLDVADFATTIWOQME----ELGMAPALQPTQGAMP 273  
QY 155 --PWORLLRKFILRSLOAFVAVAAVFAH 182  
DB 274 ASAFORRAGGVLVASHLQSFLEVSRYVLRH 303

RESULT 11  
US-08-468-609A-135  
Sequence 135, Application US/08468609A  
Patent No. 6030812  
GENERAL INFORMATION:  
APPLICANT: Abrams, Mark A.  
APPLICANT: Bauer, S. C.  
APPLICANT: Braford-Goldberg, Sarah R.  
APPLICANT: Caparon, Mair H.  
APPLICANT: Easton, Alan M.  
APPLICANT: Klein, Barbara K.  
APPLICANT: McKearn, John P.  
APPLICANT: Olin, Peter O.  
APPLICANT: Paik, Kumnan  
APPLICANT: Thomas, John W.  
TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-3)  
NUMBER OF SEQUENCES: 197  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.,  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:

```

; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-609A-135

Query Match 10.2%; Score 102; DB 3; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

QY 15 WTAQGRANPGGSS-----PAWTQCQ-----LSQKLCITLAW 45
DB 114 YVIEGRISPGGGGGSNMATPLGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYK 173
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHIQCGDQPGGLRDNQSQCFLQRIHQGLIFYE 101
DB 174 LCHPEELVLLGH-----SLGIPWAPL--SSCPSQALQ--LAGCLSQLHSGGLFLYQ 219
QY 102 KLIGSDITFG-EPSLLPDSVPAQLHASLLGLSQLLQEPGHHWETQQTIPSLSPSQ----- 154
DB 220 GLL--QALEGISPELGPGLTDLTQLDVAADFATTIWOQME-----ELGMAPALOPTQGAMPAF 273
QY 155 --PWQRLRLRKFILRSLOAFVAVAAARVFAH 182
DB 274 ASAFQRRAGGVIVASHLQSFLEVSRYVLRH 303

RESULT 12
US-08-446-872A-121
; Sequence 121, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; TITLE OF INVENTION: Fusion Protein
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESS: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-872A-121

Query Match 10.2%; Score 102; DB 4; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

QY 15 WTAQGRANPGGSS-----PAWT-----CQSQ-----LSQKLCITLAW 45
DB 114 YVIEGRISPGGGGGSNMATPLGPASSLPQSLKLEQVRKIQGDGAALQEKLCATYK 173
QY 46 SAHP-----LVGHMDLREEGDEETNDVPHIQCGDQPGGLRDNQSQCFLQRIHQGLIFYE 101
DB 174 LCHPEELVLLGH-----SLGIPWAPL--SSCPSQALQ--LAGCLSQLHSGGLFLYQ 219
QY 102 KLIGSDITFG-EPSLLPDSVPAQLHASLLGLSQLLQEPGHHWETQQTIPSLSPSQ----- 154
DB 220 GLL--QALEGISPELGPGLTDLTQLDVAADFATTIWOQME-----ELGMAPALOPTQGAMPAF 273
QY 155 --PWQRLRLRKFILRSLOAFVAVAAARVFAH 182
DB 274 ASAFQRRAGGVIVASHLQSFLEVSRYVLRH 303

RESULT 13
US-08-446-872A-122
; Sequence 122, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Mair H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; TITLE OF INVENTION: Fusion Protein
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESS: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago

```

```

; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,872A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/1
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-872A-122

```

```

Query Match      10.2%; Score 102; DB 4; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;

```

```

QY 15 WTAQGRAVPGSS-----PAWTQQQ-----LSQKLCITLAW 45
Db 114 YVIEGRISPGGGGSGNNATPLGPASSLPQSLKSLQVIRKIQGDGAALQEKLCATYK 173
QY 46 SAHP-----LVGHMDLREGEDEETNDVPHIQCGDGPQGLRDNQFCLQRIHQGLIFYE 101
Db 174 LCHPEELVLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSLQHSGLFLYQ 219
QY 102 KILGSDIFTG-EPSLLPDPSPAQLHASLLGLSOLLQPEGHWHWTQIPLSPSQ-----154
Db 220 GLL--QALEGISPGLPTLDTLQLDVADFATTIWOOME-----ELGMAPALQPTQAMPAPF 273
QY 155 --PWQRLRLRFKILRSLOAFVAVAAARVFAH 182
Db 274 ASAFQRRAGGVLVASHLQSFLEVSRYRLRH 303

```

```

RESULT 14
US-08-446-872A-134
; Sequence 134, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kumnan
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.

```

```

; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,872A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/1
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-872A-134

```

```

Query Match      10.2%; Score 102; DB 4; Length 307;
Best Local Similarity 24.8%; Pred. No. 0.0016;
Matches 52; Conservative 22; Mismatches 74; Indels 62; Gaps 11;

```

```

QY 15 WTAQGRAVPGSS-----PAWT-----QCCQ-----LSQKLCITLAW 45
Db 114 YVIEGRISPGGGGSGNNATPLGPASSLPQSLKSLQVIRKIQGDGAALQEKLCATYK 173
QY 46 SAHP-----LVGHMDLREGEDEETNDVPHIQCGDGPQGLRDNQFCLQRIHQGLIFYE 101
Db 174 LCHPEELVLGH-----SLGIPWAPL--SSCPQALQ--LAGCLSLQHSGLFLYQ 219
QY 102 KILGSDIFTG-EPSLLPDPSPAQLHASLLGLSOLLQPEGHWHWTQIPLSPSQ-----154
Db 220 GLL--QALEGISPGLPTLDTLQLDVADFATTIWOOME-----ELGMAPALQPTQAMPAPF 273
QY 155 --PWQRLRLRFKILRSLOAFVAVAAARVFAH 182
Db 274 ASAFQRRAGGVLVASHLQSFLEVSRYRLRH 303

```

```

RESULT 15
US-08-446-872A-135
; Sequence 135, Application US/08446872A
; Patent No. 6361977
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kumnan
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,  
ADDRESSEE: Corporate Patent Dept.  
STREET: P. O. Box 5110  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60680  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,872A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/192,325  
FILING DATE: 14-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bennett, Dennis A.  
REGISTRATION NUMBER: 34,547  
REFERENCE/DOCKET NUMBER: C-2790/1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)737-6986  
TELEFAX: (314)737-6972  
INFORMATION FOR SEQ ID NO: 135:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-446-872A-135

Query Match 10.2%; Score 102; DB 4; Length 307;  
Best Local Similarity 24.8%; Pred. No. 0.0016;  
Matches 52; Conservative 20; Mismatches 76; Indels 62; Gaps 10;  
QY 15 WTAQGRAVPGSS-----PAWTCQQ-----LSQKLCGLAW 45  
Db 114 YVIEGRISPGSGGSGSNMATPLGPASSLPQSFLKLSLEQVRKIQDGAALQEKLCATYK 173  
QY 46 SAHP-----LVGHMDLREGDEETNDVPHTCQGGDPPQGLRDNSQFCLQRIHQGLIFYE 101  
Db 174 LCHPEELVLGH-----SLGIPWAPL-SSCPSSQALQ--LACCLSLHSGFLFYQ 219  
QY 102 KLLGSDIFTG-EPSLLPDSVAQLHASLLGLSOLLQPEGHWHETQTIPLSPSQ-----154  
Db 220 GLL--QALEGISPELGPDTLDTQLDVAADFATTIQQME----ELGMAPALQPTQGAMPAF 273  
QY 155 --PWQRLRLRFKILRSLOAFVAVAF 182  
Db 274 ASAFQRRAGGVNASHLQSFLEVSIVRLRH 303

Search completed: November 20, 2002, 12:00:12  
Job time : 13.7818 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:35 ; Search time 14.7636 seconds  
(without alignments)  
1276.267 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLCRAVIMLWLLPWVTOGL.....AARVFAHGAATLTPLVPTA 196

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_73: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	113	10.9	208	T09216	interleukin-6 prec
2	110	10.6	208	S29549	interleukin-6 - sh
3	104	10.0	208	A56610	interleukin-6 prec
4	101.5	9.8	376	S02766	pulmonary surfacta
5	100	9.6	212	I46621	prointerleukin 6 -
6	100	9.6	212	I46590	interleukin 6 - pi
7	96	9.2	211	ICMS6	interleukin-6 prec
8	91	8.8	211	A34247	interleukin-6 prec
9	86.5	8.3	194	T09225	granulocyte colony
10	86.5	8.3	353	C96711	F24J5.9 (Imported)
11	85.5	8.2	2222	A36028	DNA-directed DNA p
12	84.5	8.1	1026	T05882	hypothetical prote
13	84	8.1	212	IVHUB2	interleukin-6 prec
14	83.5	8.0	525	1ZEBP5L	Es9 protein - pha
15	83	8.0	531	C95338	hypothetical prote
16	82.5	7.9	208	A26496	granulocyte colony
17	82.5	7.9	293	A83055	probable aminoacyl
18	82	7.9	492	T22119	hypothetical prote
19	80.5	7.8	960	S44812	F44B9.6 protein -
20	80	7.7	410	138502	gene Brn-3b protei
21	79.5	7.7	6805	S20901	titin - rabbit (fr
22	79	7.6	537	1FOMRV	gag polyprotein -
23	79	7.6	925	T29311	hypothetical prote
24	78.5	7.6	207	I46084	interleukin 6 - ca
25	78.5	7.6	530	D96810	hypothetical prote
26	78.5	7.6	797	AC3273	cell division prot
27	78	7.5	285	B83588	hypothetical prote
28	78	7.5	404	B71224	hypothetical prote
29	78	7.5	404	A75192	hypothetical prote

30	77.5	7.5	513	1	ACCHD1	nicotinic acetylch
31	77.5	7.5	1819	2	T32008	hypothetical prote
32	77	7.4	1560	2	T30282	calcium-binding pr
33	76.5	7.4	204	1	FOHUGL	granulocyte colony
34	76.5	7.4	207	2	A24573	granulocyte colony
35	76.5	7.4	331	2	S78452	POU-domain protein
36	76.5	7.4	1366	2	B86292	F7H2.12 protein -
37	76	7.3	201	2	A42247	myelomonocytic gro
38	76	7.3	411	2	I58156	Brn-3.2 - mouse
39	76	7.3	412	2	H90244	pre mRNA splicing
40	76	7.3	499	2	S22571	integrase-like pro
41	75.5	7.3	174	2	T10268	granulocyte colony
42	75.5	7.3	469	1	RGKBCP	nitrogen regulatio
43	75.5	7.3	532	2	S22262	transcription fact
44	75.5	7.3	666	2	T05432	hypothetical prote
45	75.5	7.3	822	1	TVHUFF	protein-tyrosine k

ALIGNMENTS

RESULT 1

T09216  
Interleukin-6 precursor - horse  
C:Species: Equus caballus (domestic horse)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 23-Jul-1999  
C:Accession: T09216  
R:Swiderski, C.E.; Horohov, D.W.  
submitted to the EMBL Data Library, July 1996  
A:Reference number: Z16613  
A:Accession: T09216  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-208 <SWI>  
A:Cross-references: EMBL:U64794; NID:g2654387; PID:g2654388  
C:Genetics:  
A:Gene: IL-6  
C:Superfamily: interleukin-6  
C:Keywords: cytokine; growth factor

Query Match 10.9%; Score 113; DB 2; Length 208;  
Best Local Similarity 29.4%; Pred. No. 0.0026;  
Matches 37; Conservative 22; Mismatches 51; Indels 16; Gaps 5;

QY	64	ETKNVPIQGEDGDPQGLKDNQFCLQRTQGLAPYKHLDD--SDIFKGEPLLPDSP	121
DB	84	ENNLNLPKMAEKDGCFCQSGF--NQETCLMKITGLSEFIYLEVLQNEFKGEKENTKM-	140
QY	122	MEQLHTSLGLSOLLQPEDHPRETQQMP-----LSSSQOWORPLLRSKILRSLOAF	173
DB	141	--QISTKVL-VQILMQMKNEVTPDPTAKSSLLAKLHSONEWLKNNTTTHLLIRSLDF	197
QY	174	LALAAAR	179
DB	198	LQFSLR	203

RESULT 2

S29549  
Interleukin-6 - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C:Accession: S29549  
R:Ebrahimi, B.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S29549  
A:Accession: S29549  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-208 <EBR>  
A:Cross-references: EMBL:X68723  
C:Superfamily: interleukin-6

```
Query Match          10.6%; Score 110; DB 1; Length 208;
Best Local Similarity 25.5%; Pred. No. 0.0051;
Matches 51; Conservative 27; Mismatches 84; Indels 38; Gaps 8;

QY 8 IMLWLLPWVTOGLAVPRSSSPDWAQCCQLSRNLCMLAWNAHAPAGH-----MNLRL-----E 59
Db 14 VSLGLLLVMTSAFFPGPLGEDFKNDTTPSRLLTTTPKTEALIKHIVDKISAIRKEICE 73
QY 60 EDEE-----ETKNNVPRIOCEDGCDPQGLKNSQFCIORIROGLAFYKHLID--SD 108
Db 74 KNDECSNKETIAENKLIKPKMEKDGCFQSGF--NQAVCLIKTKTAGLLEYQIYLDLFQ 131
QY 109 IFKGEFALLPDSMPMEQLHTSLGLSOLLQ-----PEDHPRETQOMPSLSSSQOWOR 159
Db 132 EFEGN-----QETVMELOQSIRTLQILAEKTAGLITTPATH---TDLLEKMQSSNEWVK 183
QY 160 PLLRSKILRSLOAFLAIAAR 179
Db 184 NAKVVIILRSLENFLQFLRLR 203

RESULT 3
A56610
interleukin-6 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R:Roogmans, L.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2, 411-413, 1992
A:Title: Nucleotide sequence of bovine interleukin-6 cDNA.
A:Reference number: A56610; MUID:93076003; PMID:1446077
A:Accession: A56610
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <DRO>
A:Cross-references: EMBL:X57317; NID:g2193; PIDN:CAA40572.1; PID:g2194
A:Experimental source: BLV induced B cell-lymphosarcoma
A:Note: sequence extracted from NCBI backbone (NCBIP:118917)
C:Superfamily: interleukin-6
C:Keywords: cytokine

Query Match          10.0%; Score 104; DB 1; Length 208;
Best Local Similarity 26.8%; Pred. No. 0.019;
Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;

QY 59 EEDE-----ETKNNVPRIOCEDGCDPQGLKNSQFCIORIROGLAFYKHLID--S 107
Db 73 EKNDCESSKETTAENKLNLPKMEKDGCFQSGF--NQACILRTTAGLLEYQIYLDYIQ 130
QY 108 DIFKGEFALLPDSMPMEQLHTSLGLSOLLQPE-----DHPRETQOMPSLSSSQOWORPL 161
Db 131 NEYESGNQENVRD-----LRKNIRTLIQILKQKIADLTITPATNTDLEKMQSSNEWVKNA 185
QY 162 LRSKILRSLOAFLAIAAR 179
Db 186 KIILILRNLENFLQFSLR 203

RESULT 4
S02766
Pulmonary surfactant protein B precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Aug-1999
R:Emrie, P.A.; Shannon, J.M.; Mason, R.J.; Fisher, J.H.
Biochim. Biophys. Acta 994, 215-221, 1989
A:Title: cDNA and deduced amino acid sequence for the rat hydrophobic pulmonary surfactant protein B.
A:Reference number: S02766; MUID:89150284; PMID:2920185
A:Accession: S02766
A:Molecule type: mRNA
A:Residues: 1-376 <EMR>
A:Cross-references: EMBL:X14778; NID:g57284; PIDN:CAA32885.1; PID:g57285
C:Superfamily: Pulmonary surfactant protein B; saposin repeat homology
```

```
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-190/Domain: propeptide #status predicted <PRO>
F;59-151/Domain: saposin repeat homology <SAP1>
F;190-277/Domain: saposin repeat homology <SAP2>
F;191-269/Domain: pulmonary surfactant protein B #status predicted <MAT>
F;286-371/Domain: saposin repeat homology <SAP3>

Query Match          9.8%; Score 101.5; DB 2; Length 376;
Best Local Similarity 29.3%; Pred. No. 0.068;
Matches 55; Conservative 22; Mismatches 70; Indels 41; Gaps 11;

QY 10 LWLPLPWVTOGLAVPRSSSPDWAQ-----COQLSRNI-----CMLAWNAHAPAGHM-- 54
Db 9 LLLLPTECLSLGATASASSPDCAQPKFWQCQSLAQTCRALGHCLQEVWGHAGANDLQC 68
QY 55 -----NLLREEDEETKNNVPRIOCEDGCDPQGLKNSQFCIORIROGLAFYKHLIDSD 108
Db 69 ECEDIVHLTLTKMTKEDAFQDTIRKFLBQECDIPLK-----LLVPRCEQVLDVYLPV-ID 123
QY 109 IFKGEFALLPDSMPMEQLHTSLGLSOLLQPEHPRETQOMPSLSSSQOWORPLLRSKILR 168
Db 124 YFQGG--IKPKAICS--HVGLCPLGQ-TKPEQKPEMLDAIPN-----PLINKLVLP 169
QY 169 SLQ-AFLA 175
Db 170 ALPGAFLA 177

RESULT 5
I46621
prointerleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46621
R:Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression
A:Reference number: I46621; MUID:9138547; PMID:1873476
A:Accession: I46621
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-212 <RIC>
A:Cross-references: GB:M86722; NID:g164624; PIDN:AAC37333.1; PID:g164625
C:Genetics:
A:Gene: IL6
C:Superfamily: interleukin-6

Query Match          9.6%; Score 100; DB 2; Length 212;
Best Local Similarity 25.0%; Pred. No. 0.047;
Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps

QY 52 GHMNLREEDE-----ETKNNVPRIOCEDGCDPQGLKNSQFCIORIROGL 98
Db 62 GKISAMRKEMCEKYKCNSEKVEIAENNLNLPKMAEKDGCQSGF--NOETCLMRITG 119
QY 99 AFYKHLID-----SDIFKGEFALLPDSMPMEQLHTSLGLSOLLQPEHPRETQOMPS--- 150
Db 120 VEFQIYLDYLOKEYESNKN-----VEAVQISTKALIQTLROKGNPKATTPNPTT 171
QY 151 -----LSSSQOWORPLLRSKILRSLOAFLAIAAR 179
Db 172 NAGLLDKLQSQNEWMKNTKIILRSLEDFLQFSLR 207

RESULT 6
I46590
interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: I46590
R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation co
```

A;Residues: 1-211 <GRE>  
A;Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728  
R;Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.  
Biochem. Biophys. Res. Commun. 166, 139-145, 1990  
A;Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleav  
A;Reference number: A90157; MUID:90147691; PMID:2302197  
A;Accession: E34047  
A:Molecule type: protein  
A;Residues: 66-69,'X','71-75;78-94;128-148 <JA5>  
R;Van Snick, J.; Cayphas, S.; Vink, A.; Uyttenhove, C.; Coulie, P.G.; Rubira, M.R.; S  
proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986  
A;Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lympho  
A;Reference number: A26662; MUID:87092311; PMID:2948184  
A;Accession: A26662  
A:Molecule type: protein  
A;Residues: 25-39,'X','41-42,'X','44-45 <VSN>  
R;Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.  
proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988  
A;Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA  
A;Reference number: A40486; MUID:89017145; PMID:3262872  
A;Accession: A40486  
A:Molecule type: mRNA  
A;Residues: 1-211 <CHI>  
A;Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410  
R;Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.  
Blood 72, 2070-2073, 1988  
A;Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleuki  
A;Reference number: A60799; MUID:89062753; PMID:3264198  
A;Accession: A60799  
A:Molecule type: protein  
A;Residues: 77-98 <SHA>  
R;Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.  
J. Exp. Med. 171, 965-970, 1990  
A;Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a  
A;Reference number: SI0241; MUID:90171860; PMID:2106569  
A;Accession: SI0241  
A;Status: preliminary  
A:Molecule type: DNA  
A;Residues: 1-6 <BLA>  
A;Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860  
R;Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.  
Eur. J. Biochem. 217, 53-59, 1993  
A;Title: Specific covalent modification of the tryptophan residues in murine interleu  
A;Reference number: S38254; MUID:94039075; PMID:8223586  
A;Accession: S38254  
A;Status: preliminary  
A:Molecule type: protein  
A;Residues: 38-60;75,'X',77-79;176-203 <ZHA>  
C;Genetics:  
A;Gene: IL-6  
A;Map position: 5  
A;Introns: 7/1; 68/3; 106/3; 156/3  
C;Superfamily: Interleukin-6  
C;Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokin  
F;1-24/Domain: signal sequence #status predicted <SIG>  
F;25-211/Product: interleukin-6 #status experimental <MA>

Query Match 9.2%; Score 96; DB 1; Length 211;  
Best Local Similarity 25.5%; Pred. No. 0.11;  
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCMLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGDCDPOGLKNSOFCLQ 92  
:::|||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||  
Db 64 EMRKEL-----NGNSDC--MN----NDDAENNLKLPEIQRNDGCYTGY--NQEICLL 111  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::||||  
QY 93 RIROGLAFYKHLD-----SDIFKGEPALLP-----DSPMEQLHTSLL--GLSQ 134  
:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
Db 112 KISSGLLEYSHYLEYMKNLNKDKNKARVLORDTETLIHFNQEVKDLHKIVLPTPISN 171  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::||||  
QY 135 LLQPEDHPRETQQMPSUSSSQWQRPRLRSKILRSLOAFIAAAR 179  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::||||  
Db 172 ALLTD-----KLESQEWLRRTTIQFIKSLEEFKVTLR 206  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::||||

```
RESULT 8
A34247
interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
R:Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derive
A:Reference number: A34247; MUID:89380206; PMID:2789217
A:Accession: A34247
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <NOR>
A:Cross-references: GB:M36744; NID:g204915; PIDN:AAA77659.1; PID:g204916
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match      8.8%; Score 91; DB 2; Length 211;
Best Local Similarity 24.5%; Pred. No. 0.33;
Matches 39; Conservative 27; Mismatches 63; Indels 30; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHNNLLREEDEETKNN--VPRIQCEGCDPQGLKDNSQFCLQ 92
Db 64 EMRKELC---NGNSDC---MN-----SDDALSENLLKLPDIQRNDCGFQGY--NQEICLL 111
QY 93 RIRQGLAFYKHLID-----SDIFKGEALLPDPSPMEQLHTSLGLSLLQQLPEDH---PR 143
Db 112 KICSGLLERFFLYEFYKNNLDKNKDKARVIOSTETLVH1----FKQEIKDSYKIVLPT 167
QY 144 ETQO-----MPSLSSQOQRPLRSKILRSIQAFIAAR 179
Db 168 PTSNALLMEKLESQEWLRTKTIQILKALEBFLKVTR 206

RESULT 9
T09255
granulocyte colony-stimulating factor precursor - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 20-Jun-2000
C:Accession: T09255
R:Dunham, S.P.; Onions, D.E.
submitted to the EMBL Data Library, September 1996
A:Description: Cloning, sequence and expression of feline granulocyte colony stimulating
A:Reference number: Z16630
A:Accession: T09255
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-194 <DUN>
A:Cross-references: EMBL:X08558
C:Function:
A:Description: stimulates the differentiation and proliferation of hematopoietic progenit
C:Superfamily: interleukin-6
C:Keywords: cytokine; growth factor; macrophage
F:1-20/domain: signal sequence (fragment) #status predicted <SIG>
F:21-194/Product: granulocyte colony-stimulating factor #status predicted <MAT>

Query Match      8.3%; Score 86.5; DB 2; Length 194;
Best Local Similarity 28.3%; Pred. No. 0.8;
Matches 34; Conservative 20; Mismatches 51; Indels 15; Gaps 5;

QY 78 CDPOGLKDNSQFCLQRIQGLAFYKHLSDIFKGEALLPDPSPMEQLHTSLGLSLLQ 137
Db 84 CSSQALQLTG--CLIRQHSGLFYQGLLQA--LAGISPELAPTLDMLQLDITDFAINWQQ 140
QY 138 PED-----HPRETQQMPSSLSSQOQRPLRSKILRSIQAFIAARFAHGAATLTTP 191
Db 141 MEDVGMAPVPPTGQTGPTTSTA--FQRRAGGTIVASNLQSFLEVAYRALRH----FTRP 194

RESULT 10
C96711
F24J5.9 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96711
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96711
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <STO>
A:Cross-references: GB:AE005173; NID:g5734711; PIDN:AAD49976.1; GSPDB:GN001
C:Genetics:
A:Gene: F24J5.9
A:Map position: 1

Query Match      8.3%; Score 86.5; DB 2; Length 353;
Best Local Similarity 26.2%; Pred. No. 1.7;
Matches 43; Conservative 20; Mismatches 48; Indels 53; Gaps 9;

QY 26 SSP-----DNAQCOQLSRNLCLAWNAHAPAGHNNLLREEDEETKNNVPRIQCEG 77
Db 104 SSPELVNKKSDMLRSVOL-----WN-HSP-----DLNPKKEERVAKKAKVYVVKPSG 150
QY 78 C-DPQGLKDNSQFCLQRIQGLAFYKHLSDIFKGEALLPDPSPMEQLHTSL-----G 131
Db 151 AFQP-----FQKRVLDTL---OPAVKVASSMPATTTSTTTETCGG 188
QY 132 LSQQLQPEDHPRETQQMPSSLSSQOQR-----PLLRSKILRSIQ 171
Db 189 KSDLIKAGDEERRIEQQSQSHTRKQRCWSPHRRFLNALQ 232

RESULT 11
A36028
DNA-directed DNA polymerase (EC 2.7.7.7) II catalytic chain - yeast (Saccharomyces ce
N:Alternate names: DNA-directed DNA polymerase II chain A; protein N0825; protein YNL
C:Species: Saccharomyces cerevisiae
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: A36028; B36028; S60919; S63235; S65121
R:Morrison, A.; Araki, H.; Clark, A.B.; Hamatake, R.K.; Sugino, A.
Cell 62, 1143-1151, 1990
A:Title: A third essential DNA polymerase in Saccharomyces cerevisiae.
A:Reference number: A36028; MUID:90381771; PMID:2169349
A:Accession: A36028
A:Molecule type: DNA
A:Residues: 1-2222 <MOR>
A:Cross-references: GB:M60416; GB:M36724; NID:g171408; PIDN:AAA88711.1; PID:g171409
A:Accession: B36028
A:Molecule type: protein
A:Residues: 1214-1216, 'X', 1218-1221 <MOR>
R:Sen-Gupta, M.; Lyck, R.; Fleig, U.; Niedenthal, R.N.; Hegemann, J.M.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of a 24152 bp segment from the left arm of chromosome XIV
A:Reference number: S60909
A:Accession: S60919
A:Molecule type: DNA
A:Residues: 1-2221 <SEN>
A:Cross-references: EMBL:X92494; NID:g1045236; PIDN:CAA63235.1; PID:g1045247
R:Sen-Gupta, M.; Lyck, R.; Niedenthal, R.K.; Fleig, U.N.; Hegemann, J.H.
submitted to the Protein Sequence Database, April 1996
A:Reference number: S63235
A:Accession: S63235
A:Molecule type: DNA
```



RESULT 13

interleukin-6 precursor [validated] - human  
N;Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-cell on factor

C;Species: Homo sapiens (man)  
C;Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 08-Dec-2000  
C;Accession: A32648; A26692; A26966; A33515; A25801; A25921; I52193; I56003; A27601;  
P;Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi,  
EMBO J. 6, 2939-2945, 1987  
A;Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g  
A;Reference number: A32648; MUID:88082684; PMID:3500852  
A;Accession: A32648  
A;Molecule type: DNA  
A;Residues: 1-212 <X>  
A;Cross-references: GB:Y00081; NID:g29494; PIDN:CAA68278.1; PID:g29495  
A;Note: the authors translated the codon CAG for residue 130 as Glu  
P;Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.  
EMBO J. 5, 2529-2537, 1986  
A;Title: Structure and expression of cDNA and genes for human interferon-beta-2, a di  
A;Reference number: A91051; MUID:87053818; PMID:3023045  
A;Accession: A25692  
A;Molecule type: mRNA  
A;Residues: 1-212 <X>  
A;Cross-references: GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674  
P;Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashiwam  
i, T.; Kishimoto, T.  
Nature 324, 73-76, 1986  
A;Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph  
A;Reference number: A93387; MUID:87065033; PMID:3491322  
A;Accession: A26966  
A;Molecule type: mRNA  
A;Residues: 1-212 <X>  
A;Cross-references: GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850  
P;Tonouchi, N.; Miwa, K.; Karsanvama, H.; Matsui, H.  
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989  
A;Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization  
A;Reference number: A33515; MUID:89391958; PMID:2789513  
A;Accession: A33515  
A;Molecule type: mRNA  
A;Residues: 1-212 <X>  
A;Cross-references: GB:M29150; NID:g186349; PIDN:AAA59154.1; PID:g307063  
P;Haegeman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.  
Eur. J. Biochem. 159, 625-632, 1986  
A;Title: Structural analysis of the sequence coding for an inducible 26-kDa protein i  
A;Reference number: A25801; MUID:87004683; PMID:3758081  
A;Accession: A25801  
A;Molecule type: DNA; mRNA  
A;Residues: 1-212 <X>  
A;Cross-references: GB:X04403  
A;Experimental source: fibroblast  
P;May, L.T.; Helfgott, D.C.; Sehgal, P.B.  
Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986  
A;Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 m  
A;Reference number: A25921; MUID:87067433; PMID:3538015  
A;Accession: A25921  
A;Molecule type: mRNA  
A;Residues: 1-212 <X>  
A;Cross-references: GB:M14584; NID:g184628; PIDN:AAA52728.1; PID:g306910

A:Wong, G.G.; Mitek Giamnotti, D.; Newick, R.R.; Chiu, J.C.; Ogawa, H.; Behring Inst. Mil. 83, 40-47, 1988  
A:Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.  
A:Reference number: I52193; MUID:89193317; PMID:3266463  
A:Accession: I52193  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-212 <GN>  
A:Cross-references: GB:M54894; NID:g186351; PIDN:AAC1704.1; PID:g186352  
R:Brakenhoff, J.P.; de Groot, E.R.; Everts, R.F.; Pannekoek, H.; Aarden, L.A.  
J. Immunol. 139, 4116-4121, 1987  
A:Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia* c  
A:Reference number: I56003; MUID:88088768; PMID:3320204  
A:Accession: I56003



Search completed: November 20, 2002, 11:55:02  
Job time : 16.7636 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:59 ; Search time 8.14545 Seconds  
(without alignments)  
998.024 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLDCAVIMLLPWTQGL.....AARVFAHGAAATLTPLVPTA 196

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	11.1	208	1 IL6_SHEEP	P29455 ovls aries
2	113	10.9	208	1 IL6_HORSE	Q95181 equus caball
3	110	10.6	208	1 IL6_CAPHI	Q28319 capra hircu
4	106.5	10.3	205	1 IL6_ORGIN	Q28747 orcinus orc
5	104	10.0	208	1 IL6_BOVIN	P26892 bos taurus
6	103	9.9	208	1 IL6_FELCA	P41683 felis silve
7	101.5	9.8	376	1 PSPB_RAT	P23355 rattus norv
8	100	9.6	212	1 IL6_PIG	P26893 sus scrofa
9	97	9.3	207	1 IL6_MOUSE	P41323 canis famil
10	96	9.2	211	1 IL6_MOUSE	P08505 mus musculu
11	91	8.8	211	1 IL6_RAT	P20607 rattus norv
12	90	8.7	209	1 IL6_PROVI	Q28819 phoca vitul
13	89.5	8.6	581	1 FRZ3_DROME	O77438 drosophila
14	89	8.6	457	1 NH20_CAEEL	Q09565 caenorhabdi
15	86.5	8.3	194	1 CSF3_FELCA	O02708 felis silve
16	86.5	8.3	195	1 CSF3_PIG	O02837 sus scrofa
17	85.5	8.2	2222	1 DPOE_YEAST	P21951 saccharomyc
18	84	8.1	212	1 IL6_HUMAN	P05231 homo sapien
19	83.5	8.0	525	1 VE53_LAMBD	P03754 bacterioph
20	82.5	7.9	208	1 CSF3_MOUSE	P09920 mus musculu
21	82.5	7.9	212	1 IL6_CERTO	P46650 cercopithec
22	82	7.9	710	1 ABB1_HUMAN	O00213 homo sapien
23	81.5	7.9	175	1 CSF3_CANFA	P35834 canis famil
24	80.5	7.8	207	1 IL6_MARMO	O35736 marmota mon
25	80.5	7.8	960	1 LI36_CAEEL	P34427 caenorhabdi
26	80	7.7	212	1 IL6_MACFA	P79341 macaca fasc
27	80	7.7	410	1 BR3B_HUMAN	Q12837 homo sapien
28	80	7.7	708	1 ABB1_MOUSE	Q9qxl1 mus musculu
29	79	7.6	537	1 GAG_MLVDR	P11269 radiation m
30	78.5	7.6	125	1 IL6_MUSVI	P41693 mustela vis
31	78.5	7.6	222	1 COLI_CYPCA	Q9yqk5 c corticotr
32	78	7.5	212	1 IL6_MACMU	P51494 macaca mula
33	77.5	7.5	513	1 ACHD_CHICK	P02717 gallus gall

ALIGNMENTS

RESULT 1

ID	IL6_SHEEP	STANDARD;	PRT;	208 AA.
AC	P29455;			
DT	01-APR-1993 (Rel. 25, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-6 precursor (IL-6).			
GN	IL6.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94041419; PubMed=8225400;			
RA	Andrews A.E., Barcham G.J., Ashman K., Meusen E.N.T., Brandon M.R.,			
RA	Nash A.D.;			
RT	"Molecular cloning and characterization of a ruminant interleukin-6			
RT	cDNA";			
RL	Immunol. Cell Biol. 71:341-348(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Ebrahimi B.;			
RL	Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL			
CC	FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION			
CC	OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND			
CC	PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN			
CC	HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X62501; CAA44363.1; -			
DR	EMBL; X68723; CAA48662.1; -			
DR	EMBL; AL9159; CAA01443.1; -			
DR	PIR; S29549; S29549.			
DR	HGSP; P05231; IL6.			
DR	InterPro; IPR003573; IL6_MGF_GCSF.			
DR	InterPro; IPR003574; Interleukin_6.			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GCSFMGF.			
DR	ProDom; PD004356; Interleukin_6; 1.			
DR	SMART; SM00126; IL6; 1.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
KW	Cytokine; Glycoprotein; Growth factor; Signal.			
FT	SIGNAL 1 29 BY SIMILARITY.			

P09919 homo sapien  
Q9yqk4 c corticotr  
P50405 mus musculu  
P13854 gallus gall  
O63934 mus musculu  
P46933 rattus norv  
Q28746 Ovis aries  
P03029 kiebsstella  
P25364 saccharomyc  
P07332 homo sapien  
P54349 bos taurus  
Q01850 homo sapien

```
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 4 L -> R (IN REF. 2).
FT CONFLICT 110 110 L -> V (IN REF. 2).
FT CONFLICT 171 171 M -> L (IN REF. 2).
FT CONFLICT 201 201 S -> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 11.1%; Score 115; DB 1; Length 208;
Best Local Similarity 25.5%; Pred. No. 0.00059;
Matches 51; Conservative 28; Mismatches 83; Indels 38; Gaps 8;

QY 8 IMWLPLPWTOGLAVPRSSPDWACQQLSRNLCMLANNAHAPAGH----MNLLR----E 59
Db 14 VSLGLLVMTSAFPTPGPLGEDFKNDTPPSRLLLTTPKTEALIKHIVDKISAIRKEICE 73
QY 60 EDE-----ETKNVPRIOCEDGCDPOGLKDNSQFCLOIRIQGLAFYKHLDD--SD 108
Db 74 KNDCEKSEKETAENKLLKLPKMEKDGCFQSGF--NQAICLIKTAGLLEQIYLDLQNL 131
QY 109 IFKGEFALLPDSPEQLHTSLGLSLLQ-----PEDHPRETOQMPSSSSQWQR 159
Db 132 EPEGN-----QETVMELOSSIRTLQILKEKTAGLITTPATH---TDMLEKMOSSNEWVK 183
QY 160 PLRSKILSLQAFIAAAR 179
Db 184 NAKVVIILRSLENFLQFSLR 203

RESULT 2
IL6_HORSE
ID IL6_HORSE STANDARD; PRT; 208 AA.
AC Q95181; O19007; O46568;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Swiderski C.E., Horohov D.W.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Leutenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lai A.C.K.;
RT "Cloning and expression of equine interleukin-6."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
```

```
DR EMBL; U64794; AAB87703.1; -.
DR EMBL; AF005227; AAB62246.1; -.
DR EMBL; AF041975; AAC04574.1; -.
DR HSP; P05231; IAL0.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin-6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT DISULFID 69 75 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 5 LS -> FF (IN REF. 1).
FT CONFLICT 8 8 T -> A (IN REF. 3).
FT CONFLICT 137 137 I -> V (IN REF. 2).
FT CONFLICT 205 205 V -> I (IN REF. 3).
SQ SEQUENCE 208 AA; 23325 MW; A62F4C234056BF66 CRC64;

Query Match 10.9%; Score 113; DB 1; Length 208;
Best Local Similarity 29.4%; Pred. No. 0.00092;
Matches 37; Conservative 22; Mismatches 51; Indels 16; Gaps 5;

QY 64 ETKNVPRIOCEDGCDPOGLKDNSQFCLOIRIQGLAFYKHLDD--SDIFKGEFALLPDS 121
Db 84 ENNLNLPKMAEKDGFQSGF--NQETCLMKITTYGLSEFYLYLQNEFKGEKENIKTM- 140
QY 122 MEQLHTSLGLSLLQLOPEDHPRETOQMPSS-----LSSSQWQRPLLSKILSLQAF 173
Db 141 --QISTKVL-VQILMQKNPEVTPDPTAKSLLAKLHSONEWLKNLTHILRSLEDF 197
QY 174 LAIAAR 179
Db 198 LQFSLR 203

RESULT 3
IL6_CAPHI
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97392354; Pubmed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells."
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```









```

QY 99 AFYKHLID-----SDIFKGEFALLPDPSPMEQLHTSLGLSLOLQEDHPRETQOMPS--- 150
DB 120 VEFQYLDYLOKEYESNKG-----VEAQVISTKALIQTLRQKGNPKATTPNPTT 171
QY 151 -----LSSQOQWRPLRLSRKILRSLOAFIAAAR 179
DB 172 NAGLLDKLOSQNEWMKNKIILILRSLEDFLOFSLR 207

RESULT 9
IL6_CANEA
ID IL6_CANEA STANDARD; PRT; 207 AA.
AC P41323;
DT 01-FEB-1995 (Rel. 31, Last Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6).
GN IL6;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mongrel;
RX MEDLINE=94303924; PubMed=7913298;
RA Kukielka G.L., Youker K.A., Hawkins H.K., Ferrard J.L.,
RA Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;
RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
RT reperfusion.";
RL Ann. N.Y. Acad. Sci. 723:258-270(1994).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U12234; AAA83030.1; -
DR HSP: P05231; IL6.
DR InterPro: IPR003573; IL6_MGF_GCSF.
DR InterPro: IPR003574; Interleukin_6.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR ProDom: PD004356; Interleukin_6; 1.
DR SMART: SM00126; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 207 INTERLEUKIN-6.
FT DISULFID 67 73 BY SIMILARITY.
FT DISULFID 96 106 BY SIMILARITY.
SQ SEQUENCE 207 AA; 22945 MW; 45540154EA9C0F50 CRC64;

Query Match 9.3%; Score 97; DB 1; Length 207;
Best Local Similarity 27.6%; Pred. No. 0.031;
Matches 43; Conservative 30; Mismatches 45; Indels 38; Gaps 10;

QY 52 GHNNLIREE-----EDEE---TKNN---VPRIQEDGCDPQGLKDNQSQFLQRIQGL 98
DB 57 GKISALRKCMDFRNCEDSKAEALNHLPLKLEKDGCFQSGF--NOETCLTRITTTGL 114
QY 99 A-FYKHL-LDSDFKGEFALLPDPSPMEQLHTSLGLSLOLQ--EDHPRETQOMPSLSS 154

```

```

DB 115 VEFQLHLNLTQNNYEGD-----KENVKSVMHSTKILVQMLKSKVKKNQDEVTTTPDPTTAS 169
QY 155 QQWORELLRSK-----ILRSLOAFIAAAR 179
DB 170 LQ---AILQSQDECVKHTTTHLILRSLEDFLOFSLR 202

RESULT 10
IL6_MOUSE
ID IL6_MOUSE STANDARD; PRT; 211 AA.
AC P08505;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Interleukin HP-1) (B-cell hybridoma
DE growth factor).
GN IL6 OR IL-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88166883; PubMed=2965020;
RA van Snick J., Cayphas S., Szikora J.-P., Renaud J.-C., van Roost E.,
RA Boon T., Simpson R.J.;
RA "cDNA cloning of murine interleukin-HP1: homology with human
RA interleukin 6.";
RL Eur. J. Immunol. 18:193-197(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89035525; PubMed=3263439;
RA Tanabe O., Akira S., Kamiya T., Wong G.G., Hirano T., Kishimoto T.;
RT "Genomic structure of the murine IL-6 gene. High degree conservation
RT of potential regulatory sequences between mouse and human.";
RL J. Immunol. 141:3875-3881(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=91057159; PubMed=2243807;
RA Grenett H.E., Fuentes N.L., Fuller G.M.;
RT "Cloning and sequence analysis of the cDNA for murine interleukin-6.";
RL Nucleic Acids Res. 18:6455-6455(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=89017145; PubMed=3262872;
RA Chiu C.P., Moulds C., Coffman R.L., Rennick D., Lee F.;
RT "Multiple biological activities are expressed by a mouse interleukin
RT 6 cDNA clone isolated from bone marrow stromal cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7099-7103(1988).
RN [5]
RP SEQUENCE OF 5-211 FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=89124383; PubMed=2563387;
RA Mock B.A., Nordan R.P., Justice M.J., Kozak C., Jenkins N.A.,
RA Copeland N.G., Clark S.C., Wong G.G., Rudikoff S.;
RT "The murine IL-6 gene maps to the proximal region of chromosome 5.";
RL J. Immunol. 142:1372-1376(1989).
RN [6]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=90171860; PubMed=2106569;
RA Blankenstein T., Qin Z., Li W., Diamantstein T.;
RT "DNA rearrangement and constitutive expression of the interleukin 6
RT gene in a mouse plasmacytoma.";
RL J. Exp. Med. 171:965-970(1990).
RN [7]
RP SEQUENCE OF 25-211.
RX MEDLINE=88329058; PubMed=3262059;
RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid
RT sequence and relation to human interleukin-6.";

```



```
ID IL6_PHOVI STANDARD; PRT; 209 AA.
AC Q28619;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-6 precursor (IL-6) (Fragment).
GN IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Phoca.
OX NCBI_TaxID=9720;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel D.A., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Ferrick M.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO Ig-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L46802; AAB01430.1; -
DR HSSP; P05231; IL6.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PRODOM; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR KEGG; Glycopolterin; Growth factor; Signal.
FT NON_TER 1
FT SIGNAL <1 26 BY SIMILARITY.
FT CHAIN 27 209 INTERLEUKIN-6.
FT DISULFID 69 75 BY SIMILARITY.
FT DISULFID 98 108 BY SIMILARITY.
SQ SEQUENCE 209 AA; 23483 MW; 75144922E43B48E9 CRC64;
Query Match 8.7%; Score 90; DB 1; Length 209;
Best Local Similarity 27.3%; Pred. No. 0.15;
Matches 42; Conservative 25; Mismatches 53; Indels 34; Gaps 10;
QY 52 GHMNLREE-----EDEE---TKNN---VPRIQEDGCDPQGLKDNQSFCLQIRIQG- 97
Db 59 GKTISALRKEMCDKYNKCEDSKAEALNNRLPKLAEKDGFQSGF--NOETCLTRITGL 116
QY 98 LAFYKHL--LDSDIFKGEPAALLPDSPEWQLHTSLGLSLLQLQPE-----DHPRET 145
Db 117 LEFQHLKLYIQAN-YEGNK---EDANSVYISTKL--LVQMLMKVKKSQDEVITPDTTDT 170
QY 146 QQPSLSSSQWQORPLRLSKILRSLSQAFIAAAR 179
Db 171 SLQAILRAQDKWLKHTTHILKLSLEDFLQFSLR 204
RESULT 13
FRZ3_DROME
ID FRZ3_DROME, STANDARD; PRT; 581 AA.
```

```
AC O77438; Q91727; Q9NIU0; Q9U902; Q9W5D5;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Frizzled protein 3 precursor (Frizzled-3) (DFz3).
GN FZ3 OR EG:34F3.6 OR CG16785.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=99429803; PubMed=10498678;
RA Sato A., Kojima T., Ui-Tel K., Miyata Y., Saigo K.;
RT "Dfrizzled-3, a new Drosophila Wnt receptor, acting as an attenuator
RT of Wingless signaling in wingless hypomorphic mutants.";
RL Development 126:4421-4430(1999).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND FUNCTION.
RX MEDLINE=20171076; PubMed=10704878;
RA Sivasankaran R., Calleja M., Morata G., Basler K.;
RT "The Wingless target gene Dfz3 encodes a new member of the Drosophila
RT Frizzled family.";
RL Mech. Dev. 91:427-431(2000).
RN [3]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX STRAIN-Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demallies J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablo B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikoti F.,
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitson A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valentini P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster.";
RL Science 287:2220-2222(2000).
RN [4]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
RX STRAIN-Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Iqbal C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
```

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:  
RA "The genome sequence of *Drosophila melanogaster*.";  
RL Science 287:2185-2195(2000).  
CC -|- FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors  
CC are coupled to the beta-catenin canonical signaling pathway, which  
CC leads to the activation of dishevelled proteins, inhibition of  
CC GSK-3 kinase, nuclear accumulation of beta-catenin and activation  
CC of Wnt target genes. A second signaling pathway involving PKC and  
CC calcium fluxes has been seen for some family members, but it is  
CC not yet clear if it represents a distinct pathway or if it can be  
CC integrated in the canonical pathway, as PKC seems to be required  
CC for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem  
CC to involve interactions with G-proteins. Required to coordinate  
CC the cytoskeletons of epidermal cells to produce a parallel array  
CC of cuticular hairs and bristles.  
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
CC -|- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a  
CC short form; are produced by alternative splicing.  
CC -|- TISSUE SPECIFICITY: Wing, leg and eye imaginal disks. In embryos,  
CC expressed is seen in brain, proventriculus, Malpighian tubules,  
CC anal plate and visceral mesoderm of parasegment 8.  
CC -|- DEVELOPMENTAL STAGE: Expressed in embryos from stage 11 and in  
CC larvae.  
CC -|- DOMAIN: The fz domain is involved in binding with Wnt ligands (By  
CC similarity).  
CC -|- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED  
CC RECEPTORS.  
CC -|- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AB018565; BAA84677.1; -;  
DR EMBL; AF195242; AAF63250.1; -;  
DR EMBL; AL031583; CAA20896.1; -;  
DR EMBL; AF003418; AAF45547.1; -;  
DR EMBL; AB003418; AAG22363.1; -;  
DR FlyBase; FBgn0027343; fz3  
DR InterPro; IPR000539; Frizzled.  
DR InterPro; IPR000024; Fz.domain.  
DR Pfam; PF01534; Frizzled; 1.  
DR Pfam; PF01392; Fz; 1.  
DR PRINTS; PR00489; FRIZZLED.  
DR SMART; SM00063; FRI; 1.  
DR PROSITE; PS50038; FZ; 1.  
DR PROSITE; PS50261; G-PROTEIN\_RECEP\_F2\_4; 1.  
KW Multigene family; Receptor; G-protein coupled receptor; Transmembrane;  
KW Developmental protein; Glycoprotein; signal; Alternative splicing.  
FT SIGNAL 1 19 POTENTIAL  
FT CHAIN 20 581 FRIZZLED PROTEIN 3.  
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 238 258 1 (POTENTIAL).  
FT DOMAIN 259 270 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 271 291 2 (POTENTIAL).  
FT DOMAIN 292 321 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 322 342 3 (POTENTIAL).  
FT DOMAIN 343 359 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 360 380 4 (POTENTIAL).  
FT DOMAIN 381 393 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 394 414 5 (POTENTIAL).  
FT DOMAIN 415 442 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 443 463 6 (POTENTIAL).  
FT DOMAIN 464 488 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 489 509 7 (POTENTIAL).  
FT DOMAIN 510 581 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 581 581 FZ.  
FT DOMAIN 35 156 POLY-LEU.  
FT SITE 403 410 PDZ-BINDING.  
FT CARBOHYD 579 581 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT CARBOHYD 54 54 N-LINKED (GLCNAC. .) (POTENTIAL).  
FT TRANSMEM 206 206 MISSING (IN SHORT ISOFORM).  
FT VARSPLIC 1 55 TALPNLGHNTQLAEQLQ -> MDKKTKEVCVEGLDYLIP  
FT VARSPLIC 56 73 (IN SHORT ISOFORM).  
FT CONFLICT 56 56 T -> I (IN REF. 1).  
FT CONFLICT 192 192 A -> V (IN REF. 1).  
FT CONFLICT 276 276 L -> P (IN REF. 1).  
FT CONFLICT 304 304 G -> W (IN REF. 4).  
FT CONFLICT 376 376 A -> V (IN REF. 1).  
SQ SEQUENCE 581 AA; 63251 MW; 07A8BBFF2A9E3F93 CRC64;  
Query Match 8.6%; Score 89.5; DB 1; Length 581;  
Best Local Similarity 29.0%; Pred. No. 0.59;  
Matches 45; Conservative 23; Mismatches 60; Indels 27; Gaps 10;  
QY 6 AVIMLWLLPWVWTQGLA-----VPRSSPDWAQCOQLSRNLCM-LAWNAHA---PAG 52  
DB 4 ASILLHLTWAVATTAANGAGHGPVASCAGPGLQCQGLVNTALPNLJAG 63  
QY 53 HMNLLREDEETKNNVPRIQCDCDPQG--LKDNSOF--CLQRIQGLAFYKHLSD 108  
DB 64 HTNQL--EAEQLQAKLVPLI--ESGCSRRARFLLCSSLPFLCTPDVPRPVAACKLLCET- 118  
QY 109 IFKGPALLPSPME--QLHTSLILGLSLOLQPEDH 141  
DB 119 -VRGE--CMENAPPPELMELWPSFLNCDGLPQPEKH 150  
RESULT 14  
ID NH20\_CAEEL STANDARD; PRT; 457 AA.  
AC Q09565; O9GTI6;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Nuclear hormone receptor family member nhr-20.  
GN NHR-20 OR F43C1.4.  
OS *Caenorhabditis elegans*.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peioderinae; *Caenorhabditis*.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RA Jassal B., Smith A.;  
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP REVISIONS.  
RA Durbin R.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 4-457 FROM N.A.  
RA Bogan A., Maina C.V., Yamamoto K., Cohen F., Sluder A.E.;  
RT "Caenorhabditis elegans nuclear receptor sequences exhibit biophysical  
RL compatibility with the ligand-binding domain fold".  
CC Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -|- FUNCTION: ORPHAN NUCLEAR RECEPTOR.  
CC -|- SUBCELLULAR LOCATION: Nuclear (potential).  
CC -|- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:51:20 ; Search time 26.9818 Seconds  
(without alignments)  
1496.757 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLCRAVIMLWLLPWVTQGL.....AARVFAHGAATLTPVLVPTA 196

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_21.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	1038	100.0	196	11 Q9EQ14	Q9eq14 mus musculus
2	915	88.2	196	11 Q91Z84	Q91z84 rattus norv
3	718.5	69.2	189	4 Q9H2A5	Q9h2a5 homo sapien
4	717.5	69.1	189	4 Q9NPF7	Q9npf7 homo sapien
5	663.5	63.9	193	6 Q9N2H9	Q9n2h9 sus scrofa
6	113.5	10.9	208	6 Q9XT80	Q9xt80 delphinapte
7	106	10.2	207	6 Q9WVZ7	Q9wvz7 canis famli
8	98	9.4	212	11 Q91ZL3	Q91z13 sigmodon hi
9	95	9.2	210	11 Q9WVQ8	Q9wvq8 mesocricetu
10	91	8.8	209	6 Q9TTH3	Q9tth3 aotus lemur
11	90	8.7	241	6 Q9MZR1	Q9mzr1 oryza sativ
12	89.5	8.6	1217	10 Q94I37	Q94i37 oryza sativ
13	89	8.6	4306	11 Q9J7J9	Q9j7j9 rattus norv
14	86.5	8.3	195	6 Q9GJU0	Q9gju0 felis silve
15	86.5	8.3	353	10 Q9SX30	Q9sxx30 arabidopsis
16	86.5	8.3	354	10 Q9VZS3	Q9vzs3 arabidopsis

17	84.5	8.1	432	10 Q9FHP0	Q9fhp0 arabidopsis
18	84.5	8.1	1026	10 Q49529	Q49529 arabidopsis
19	84	8.1	209	6 Q97540	Q97540 aotus nancy
20	83	8.0	207	6 Q28403	Q28403 enhydra lut
21	83	8.0	508	5 Q8T012	Q8t012 drosophila
22	83	8.0	531	16 Q92Z81	Q92z81 rhizobium m
23	83	8.0	857	5 Q9V624	Q9v624 drosophila
24	82.5	7.9	293	16 Q9HV75	Q9hv75 pseudomonas
25	82	7.9	708	4 Q96A93	Q96a93 homo sapien
26	82	7.9	712	4 Q8TEY4	Q8tey4 homo sapien
27	81	7.8	652	5 Q77168	Q77168 apis mellif
28	80.5	7.8	241	13 Q90Y10	Q90y10 gallus gall
29	80.5	7.8	962	5 Q9U552	Q9u552 caenorhabdi
30	80	7.7	603	16 Q8XXA0	Q8xxa0 talstonia s
31	80	7.7	1011	4 Q9H0F4	Q9h0f4 homo sapien
32	80	7.7	1731	4 Q8TEP8	Q8tep8 homo sapien
33	79.5	7.7	953	2 Q9L4W0	Q9l4w0 streptomyce
34	79.5	7.7	6875	6 Q28733	Q28733 oryctolagus
35	79	7.6	108	6 Q9BDL5	Q9bd15 phocoenoide
36	79	7.6	557	11 Q91WJ7	Q91wj7 mus musculu
37	79	7.6	558	11 Q8VC37	Q8vc37 mus muscul
38	79	7.6	605	2 Q8VT81	Q8vt81 agrobacteri
39	79	7.6	1833	5 Q95ZU1	Q95zul caenorhabdi
40	79	7.6	1835	5 Q95ZU2	Q95zu2 caenorhabdi
41	79	7.6	1839	5 Q17383	Q17383 caenorhabdi
42	78.5	7.6	207	11 Q9JHH3	Q9jhh3 marmota mon
43	78.5	7.6	530	10 Q9C9S0	Q9c9s0 arabidopsis
44	78.5	7.6	797	16 Q8YJ88	Q8yjb8 bruceella me
45	78	7.5	285	16 Q9I649	Q9i649 pseudomonas

#### ALIGNMENTS

RESULT 1

Q9EQ14  
ID Q9EQ14 PRELIMINARY; PRT; 196 AA.  
AC Q9EQ14;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE Interleukin 23 p19 subunit (Interleukin 23, alpha subunit p19).  
GN IL23A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
RX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20567322; PubMed=11114383;  
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,  
RA Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,  
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,  
RA Moore K.W., Rennick D., de Waal-Malefyt R., Hannum C., Bazan J.F.,  
RA Kastelein R.A.;  
RT "Novel p19 Protein Engages IL-12p40 to Form a Cytokine, IL-23, with  
RT Biological Activities Similar as Well as Distinct from IL-12";  
RL Immunity 13:715-725(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF301619; AAC37231.1; -;  
DR EMBL; BC019953; AAH19953.1; -;  
DR MGD; MGI:1932410; IL23a.  
DR InterPro; IPR003573; IL6\_MGF\_GCSF.  
DR SMART; SM00126; IL6; 1  
SQ SEQUENCE 196 AA; 22071 MW; DAF4A318A2DD3B7C CRC64;

Query Match 100.0%; Score 1038; DB 11; Length 196;  
Best Local Similarity 100.0%; Pred. No. 2e-101;  
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
QY 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
QY 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
QY 181 FAHGAATLTPVPTA 196
|||
DB 181 FAHGAATLTPVPTA 196
|||
RESULT 2
Q91284 PRELIMINARY; PRT; 196 AA.
AC Q91284;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE Interleukin 23.
DE Interleukin 23.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW.
RA Tran G., Hodgkinson S.;
RT "Rattus norvegicus il-23 mRNA.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY05379; AAL18229.1; -.
SQ SEQUENCE 196 AA; 21986 MW; 188FF74BC409A961 CRC64;

Query Match 88.2%; Score 915; DB 11; Length 196;
Best Local Similarity 87.8%; Pred. No. 1.9e-88;
Matches 172; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
QY 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
QY 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
QY 181 FAHGAATLTPVPTA 196
|||
DB 181 FAHGAATLTPVPTA 196
|||
RESULT 3
Q9H2A5 PRELIMINARY; PRT; 189 AA.
AC Q9H2A5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Interleukin 23 p19 subunit.
DE Interleukin 23 p19 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RX MEDLINE=20567322; PubMed=11114383;
RA Oppmann B., Lesley R., Blom B., Timans J.C., Xu Y., Hunte B., Vega F.,
Yu N., Wang J., Singh K., Zonin F., Vaisberg E., Churakova T.,
RA Liu M.-R., Gorman D., Wagner J., Zurawski S., Liu Y.-J., Abrams J.S.,
RA Moore K.W., Rennick D., de Waal-Maleijt R., Hannum C., Bazan J.F.,
RA Kastelein R.A.;
RT "Novel p19 protein engages IL-12p40 to form a cytokine, IL-23, with
RT Biological Activities Similar as Well as Distinct from IL-12.";
RL Immunity 13:715-725(2000);
DR EMBL; AF301620; AAG37232.1; -.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 189 AA; 20744 MW; BFB5C0F42D4CIE3A CRC64;

Query Match 69.2%; Score 718.5; DB 4; Length 189;
Best Local Similarity 74.6%; Pred. No. 9.3e-68;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
QY 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
QY 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
QY 181 FAHGAATLTPVPTA 189
|||
DB 181 FAHGAATLTPVPTA 189
|||
RESULT 4
Q9NPF7 PRELIMINARY; PRT; 189 AA.
AC Q9NPF7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE SGRF precursor.
DE SGRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN;
RA Hirata Y., Kosuge Y.;
RT "SGRF: a novel member of the IL-6/G-CSF family.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030000; BAA93886.1; -.
DR EMBL; AB030001; BAA93687.1; -.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR SMART; SM00126; IL6; 1.
KW Signal.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 189 SGRF.
SQ SEQUENCE 189 AA; 20730 MW; 51B5C0F188EC1B9F CRC64;

Query Match 69.1%; Score 717.5; DB 4; Length 189;
Best Local Similarity 74.6%; Pred. No. 1.2e-67;
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
DB 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60
|||
QY 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
DB 61 EDEETKNNVPRIQCEGCDGCDPQGLKDNSQFCQRIROGLAFYKHLSDIFKGEFALLPDS 120
|||
QY 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
DB 121 PMEQLHTSLGLSOLLQLOPEDHPRETQOMPSLSSSQOWORPLRLSKILRSLOAFIAAARV 180
|||
QY 181 FAHGAATLTPVPTA 189
|||
DB 181 FAHGAATLTPVPTA 189
|||
RESULT 5
Q9H2A5 PRELIMINARY; PRT; 189 AA.
AC Q9H2A5;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DE Interleukin 23 p19 subunit.
DE Interleukin 23 p19 subunit.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
```







```
Q9MZRI ID Q9MZRI PRELIMINARY; PRT; 241 AA.
AC Q9MZRI;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Interleukin 6
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, AND LYMPH NODE;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
DR EMBL; AF169176; AAF86660.1; -.
DR HSP; P05231; IL6.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR InterPro; IPR003574; Interleukin_6.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD004356; Interleukin_6; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; UNKNOWN.1.
SQ SEQUENCE 241 AA; 27021 MW; 781D323692C3EE97 CRC64;

Query Match 8.7%; Score 90; DB 6; Length 241;
Best Local Similarity 23.8%; Pred. No. 0.22;
Matches 46; Conservative 25; Mismatches 70; Indels 52; Gaps 8;

QY 34 QQLSRNLCLANAHAPAGHMLNLRREEDEETKNNVPRIQCDCDQGLKNDNSQFCQOR 93
DB 65 KELKEMCDHVN-----MN--RKEALAEVNLHLPLRIEEDGCFPAV--NNETCLLR 114
QY 94 IROGLAFYKHLLD-----SDIFKGPALLPDSPMQHLTSLGLSQ--LL 136
DB 115 ITSLMEFRMYLEHLQAKFRSDEENTRVSMVLKNIOHLI-----KTLRPKVKLNLEEATL 169
QY 137 OPEDHPRETQQPWSLSSSQWOPRLRSKILRSLOAFLAIAARVE----- 181
DB 170 KP---AVAVSLMENQQKNQWLKTTIHFILRGLNFLEFTLRAVDLMEECCPLRNFPMG 226
QY 182 --AHGAATLTPEL 192
DB 227 SASHGQNTFSCPL 239

RESULT 12
Q94I37 ID Q94I37 PRELIMINARY; PRT; 1217 AA.
AC Q94I37;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative retroelement.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Rodriguez M.A., de la Bastide M.,
RA Preston R.R., Nascimento L.U., King L., Kirchoff K.A., Vil M.D.,
RA Baker J.P., Miller B., Toth K., Shah R.S., Bal H., O'Shaughnessy A.,
RA Dedhia N.N., McCombie W.R.;
RT "Genomic Sequence For Oryza sativa, Nipponbare Strain, Chromosome X,
RT Clone OSJNbA050N08, Complete Sequence.";
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
```

```
RN [2]
RP SEQUENCE FROM N.A.
RA McCombie W.R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Palmer L.E., Bal H., Spiegel L.A., Huang E.N., Rodriguez M.A.,
RA de la Bastide M., Preston R.R., Nascimento L.U., King L.,
RA Kirchoff K.A., Vil M.D., Baker J.P., Miller B., Toth K., Shah R.S.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Palmer L.E., Bal H., Spiegel L.A., Huang E.N., Rodriguez M.A.,
RA de la Bastide M., Preston R.R., Nascimento L.U., King L.,
RA Kirchoff K.A., Vil M.D., Baker J.P., Miller B., Toth K., Shah R.S.,
RA O'Shaughnessy A., Dedhia N.N., McCombie W.R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC021891; AAK50412.1; -.
DR InterPro; IPR001584; Rve.
DR InterPro; IPR001878; Znf_CCHC.
DR Pfam; PF00665; rve; 1.
DR Pfam; PF00098; zf-CCHC; 1.
SQ SEQUENCE 1217 AA; 134726 MW; 36B9BD25FE629743 CRC64;

Query Match 8.6%; Score 89.5; DB 10; Length 1217;
Best Local Similarity 28.2%; Pred. No. 1.9;
Matches 37; Conservative 20; Mismatches 37; Indels 37; Gaps 8;

QY 14 PWTGGLAVPRSSPDWAQCOOLSRNLCML-----ANNAHAPAGHMLN--LREEDEET 65
DB 448 PW-RLVMKVRRTSNLYRIEQLQSLASLDNPAWMLHGHVNFHAKLLVDKEM 506
QY 66 KNNVPRIQCDCDQGLKNDNSQFCQ--QRIQ---GLAFYKHLLDSDIFKGPALLPDS 120
DB 507 ASSVPTVH-----HFNQL---CQACLVAQVQRPFGMANVR-----AEA 543
QY 121 PMEQHLTSLG 131
DB 544 PLELLHMDLGC 554

RESULT 13
Q9JJ79 ID Q9JJ79 PRELIMINARY; PRT; 4306 AA.
AC Q9JJ79;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Cytoplasmic dynein heavy chain.
GN DNHC2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;
RA Mikami A.;
RT "Molecular analysis of cytoplasmic dynein.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE DAWLEY; TISSUE=TESTIS;
RA Mikami A., Vallee R.B.;
RT "In vitro expression of enzymatically active cytoplasmic dynein heavy
RT chain fragments.";
RL Mol. Biol. Cell 9:276-276(1998).
DR EMBL; AB041881; BAA97048.1; -.
DR InterPro; IPR004273; Dynein_heavy.
DR Pfam; PF03028; Dynein_heavy; 1.
SQ SEQUENCE 4306 AA; 492206 MW; A4AC9B7B9E7FA330 CRC64;
```

```
Query Match      8.6%; Score 89; DB 11; Length 4306;
Best Local Similarity 28.0%; Pred. No. 10;
Matches 40; Conservative 20; Mismatches 55; Indels 28; Gaps 8;

QY 53 HNNLLREEDDEETKNNPRIQEDGCDPQGLKDNSQFCL--QRIRQGLAFYKHLHDS-- 108
Db 20 YFGLRPELMDQTPLSNCPVW-----NFLDDGNQMLLRVQSRDAGLAF-SNTIDFDT 71

QY 109 -----IFKGEFALLPDSPEQLHTSLGLSOLLQPEDHPRETOOM---PSLSSSQWQR 159
Db 72 KDKVLVFFKLREPVITDG---NLHTNILVSSLMESPINSLYQAVRQVFAPMLLKQDEWSR 128

QY 160 ---PLLRSKILRSLOAFIAIAR 179
Db 129 NFDPKLQN-LLSELAGGVLR 150

RESULT 14
Q9GUUO PRELIMINARY; PRT; 195 AA.
AC Q9GUUO;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Granulocyte colony-stimulating factor precursor.
GN G-CSF.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RA Yamanoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K.,
RA Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RA Yamanoto A., Iwata A., Tuchiya K., Katsumata A., Oishi K., Saito T.,
RA Tsujimoto H., Hasegawa A., Ueda S.;
RT "Molecular cloning and expression of the cDNA encoding feline
RT granulocyte colony-stimulating factor.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB042552; BAB17789.1; -.
DR EMBL; AB042553; BAB17757.1; -.
DR HSSP; P35834; 1BGE.
DR InterPro; IPR003629; GCSF_MGF.
DR InterPro; IPR003573; IL6_MGF_GCSF.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR ProDom; PD008388; GCSF_MGF; 1.
DR SMART; SM00126; IL6; 1.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 195 AA; 21255 MW; 544C682909412PCF CRC64;

Query Match      8.3%; Score 86.5; DB 6; Length 195;
Best Local Similarity 28.3%; Pred. No. 0.4;
Matches 34; Conservative 20; Mismatches 51; Indels 15; Gaps 5;

QY 78 CDPQGLKDNSQFCLQRIROGLAFYKHLHDSIDIFKGEFALLPDSPEQLHTSLGLSOLLQ 137
Db 85 CSSQALQITG-CLRLQHSGLFLYQGLLQA-LAGISPELAPTLDMQLQDITDFAINIQW 141

QY 138 PED-----HPRETOQMPSSLSSSQWQRLLRSKILRSLOAFIAIARVFAHCAATLTER 191
Db 142 MEDYGMAPVPPQTGTMTPTSA--FORRAGGTLVASNLQSFLEVAYRALRH-----FTKP 195

RESULT 15
Q9SX30 PRELIMINARY; PRT; 353 AA.
AC Q9SX30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE F24J5.9.
GN F24J5.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euraids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RA STRAIN=CV. COLOMBIA;
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Lee J.M., Li J., Gonzalez A., Liu A., Vaysberg M., Sakano H.,
RA Chin C., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
RA Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
RA Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC008075; AAD49976.1; -.
SQ SEQUENCE 353 AA; 39293 MW; DE6DCDAFC6EC4A0C CRC64;

Query Match      8.3%; Score 86.5; DB 10; Length 353;
Best Local Similarity 26.2%; Pred. No. 0.84;
Matches 43; Conservative 20; Mismatches 48; Indels 53; Gaps 9;

QY 26 SSP-----DWAQCOQLSRNLCMLAWNAHAPAGHMNLLREDEETKNNVPRICEDG 77
Db 104 SSPELVNNKSDWLRVQL-----WN-HSP-----DLNPKERVAKKAKVVEVKPSG 150

QY 78 C-DPQGLKDNSQFCLQRIROGLAFYKHLHDSIDIFKGEFALLPDSPEQLHTSL--G 131
Db 151 AFQP-----FQKRVLETDL---QPAVKVASSMPATTTSTTETCGG 188

QY 132 LSQQLQPEDHPRETOQMPSSLSSSQWQR---PLLRSKILRSLO 171
Db 189 KSDLIKAGDEERRIEQQSQSQSHTRKQRRCWSPELHRRFLNALQ 232

Search completed: November 20, 2002, 11:54:26
Job time : 28.9818 secs
```

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:48:39 ; Search time 33.6 seconds  
(without alignments)  
777.295 Million cell updates/sec

Title: US-09-658-699-4

Perfect score: 1038

Sequence: 1 MLCRAVIMLWLLPWVTOGL.....AARVFAHGAATTEPLVPTA 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_101002.\*

1:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20:	/SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23:	/SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1038	100.0	196	20	Mouse interleukin
2	1038	100.0	196	20	Mouse interleukin
3	1038	100.0	196	21	Murine interleukin
4	1038	100.0	196	22	Murine IL-B30. Mu
5	718.5	69.2	189	20	Human interleukin
6	718.5	69.2	189	20	Human interleukin
7	718.5	69.2	189	21	Human interleukin
8	718.5	69.2	189	22	Human IL-B30. Hom
9	717.5	69.1	189	21	Human secreted pro
10	717.5	69.1	189	21	SGRF protein seque

11	717.5	69.1	189	22	AAU12287	Human PR05798 poly
12	717.5	69.1	189	22	AAB48070	Human extracellular
13	356	34.3	102	20	AAZ29787	Partial pig interl
14	356	34.3	102	20	AAW95004	Pig interleukin-B3
15	356	34.3	102	21	AA801983	Mature porcine int
16	115	11.1	208	13	AAZ22125	Sequence of ovine
17	112	10.8	181	13	AAZ22128	Sequence of ovine
18	112	10.8	184	20	AAW95012	Sheep interleukin
19	104	10.0	208	22	AAW99342	Bovine interleukin
20	96	9.2	188	20	AAW95013	Mouse interleukin
21	96	9.2	211	14	AAW93385	Cytokine mIL-6. M
22	96	9.2	211	15	AAW90400	Murine interleukin
23	92.5	8.9	186	14	AAW93197	Met-IL-6 SSCC mute
24	92.5	8.9	186	15	AAW93197	Human interleukin
25	92.5	8.9	186	17	AAW05587	SSCC mutein of hum
26	91	8.8	211	11	AAW06847	Rat interleukin-6
27	89.5	8.6	581	22	ABW68074	Drosophila melanog
28	89	8.6	212	14	AAW93384	Cytokine hIL-6. H
29	89	8.6	212	22	AAW93384	Human interferon b
30	88	8.5	181	22	AAW16191	Human novel seque
31	88	8.5	181	22	AAW16606	Segment of B-cell
32	88	8.5	185	11	AAW05311	Full length interl
33	88	8.5	185	15	AAW45718	Human mutant IL-6a
34	87.5	8.4	162	16	AAW77391	Human interleukin
35	87.5	8.4	163	17	AAW00132	Human IL-6 mutant
36	87.5	8.4	177	16	AAW77388	Human interleukin
37	86.5	8.3	162	17	AAW00131	Human interleukin
38	86.5	8.3	174	20	AAW95006	Feline G-CSF seque
39	86.5	8.3	195	20	AAW02471	A granulocyte colo
40	86.5	8.3	309	22	ABG15321	Novel human diagno
41	86.5	8.3	319	16	AAW80147	Chimeric interleuk
42	86.5	8.3	337	16	AAW79324	IL-3 containing fu
43	86.5	8.3	337	21	AAW53205	Human interleukin
44	86.5	8.3	337	22	AAW13999	Myelopietin (MPO)
45	86.5	8.3	347	19	AAW78103	Chimeric receptor

#### ALIGNMENTS

##### RESULT 1

AAZ29784  
ID AAZ29784 standard; Protein; 196 AA.

XX AC

XX AC

XX 04-NOV-1999 (first entry)

DE Mouse interleukin B30.

DE Mouse interleukin B30.

XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;

XX interleukin B30; DSR1; DCRL; IL-B30; cytokine receptor; diagnosis;

KW inflammatory disorder; inflammatory response; innate immunity;

KW morphogenic development; immunological disorder.

XX Mus sp.

OS Mus sp.

XX Key

XX Peptide

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein

XX Protein



inflammatory disease; autoimmune disease; antigen; antibody.

Mus sp.

Key Location/Qualifiers  
 Peptide 1..21  
 Protein /note= "Signal peptide"  
 /note= "Mature murine IL-B30"

US06060284-A.

09-MAY-2000.

24-JUL-1998; 98US-0122443.

25-JUL-1997; 97US-0053765.

(SCHE ) SCHERING CORP.

Bazan JF;

WPI; 2000-364420/31.  
 N-PSDB; AAA52578.

Novel recombinant DNA encoding cytokines especially interleukin-B30 useful as probes or primers for diagnosing immune disorders including autoimmune or chronic inflammatory conditions -

Claim 1; Column 7-10; 32pp; English.

This sequence represents murine interleukin-B30 (IL-B30). IL-B30 is a novel cytokine, exhibiting significant homology to IL-6 and GCSF (granulocyte colony stimulating factor). Cytokines play a critical role in signalling between immune or other cells during an immune response. The precise role of IL-B30 is not yet known - it is likely to have either a stimulatory or an inhibitory effect on haematopoietic cells such as T-cells, B-cells, natural killer (NK) cells and macrophages. Alternatively, it may affect vascular physiology or development, or have neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and antagonists are useful in the diagnosis and treatment of disorders associated with abnormal expression or activity of IL-B30 e.g., inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are useful for recombinant expression of IL-B30 in a host cell, and as a source of probes and primers. The IL-B30 probes and primers can be used to detect levels of IL-B30 expression in samples from patients suspected of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may also be used to identify homologous genes in other species. IL-B30 protein or its fragments are useful as antigens for raising antibodies to various linear and conformational epitopes. Such antibodies may be used to detect levels of IL-B30 protein in a sample.

Sequence 196 AA;

Query Match 100.0%; Score 1038; DB 21; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-99;  
 Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLCRAVIMLWLPWYTOGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMNLLREE 60  
 |||||  
 Db 1 MLCRAVIMLWLPWYTOGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMNLLREE 60

QY 61 EDEETNNVRIQCEGCDPQGLKDNSQFCLOIRIQGLAFYKHLSDIFKGEPAALLPDS 120  
 |||||  
 Db 61 EDEETNNVRIQCEGCDPQGLKDNSQFCLOIRIQGLAFYKHLSDIFKGEPAALLPDS 120

QY 121 PMEQLHTSLGLSQLLQPEDHPRETQMPSLSSSQWQRPRLRSKILRSQAFLAIAARV 180  
 |||||  
 Db 121 PMEQLHTSLGLSQLLQPEDHPRETQMPSLSSSQWQRPRLRSKILRSQAFLAIAARV 180

QY 181 FAHGAATLTLEPLVPTA 196  
 |||||  
 Db 181 FAHGAATLTLEPLVPTA 196

RESULT 4  
 AAB47121  
 ID AAB47121 standard; Protein; 196 AA.  
 XX  
 AC AAB47121;  
 XX  
 DT 04-JUN-2001 (first entry)  
 XX  
 DE Murine IL-B30.  
 XX  
 Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
 IFNgamma; Th1 response; autoimmune disease; chronic inflammation;  
 KW memory T-cell; leukocyte; rheumatoid arthritis; osteoarthritis;  
 KW atherosclerosis; multiple sclerosis; vasculitis; spinal injury;  
 KW delayed hypersensitivity; skin graft; transplant; cancer; tumour;  
 KW stroke; neurodegeneration; ischaemia; postmenopausal osteoporosis;  
 KW Castleman's disease.  
 XX  
 Mus musculus.  
 OS  
 XX  
 Key Location/Qualifiers  
 FH Peptide 1..21  
 FT /note= "Signal peptide"  
 FT Protein 22..196  
 FT /note= "Mature protein"  
 XX  
 WO200118051-A2.  
 XX  
 15-MAR-2001.  
 XX  
 08-SEP-2000; 2000WO-US24686.  
 XX  
 09-SEP-1999; 99US-0393090.  
 PR 10-NOV-1999; 99US-0164616.  
 XX  
 (SCHE ) SCHERING CORP.  
 XX  
 Oppmann B, De Waal Malefyt R, Rennick DM, Kastelein RA;  
 PI Wiekowski MT, Lira SA, Narula SK;  
 XX  
 WPI; 2001-244560/25.  
 DR N-PSDB; AAC85541.  
 XX  
 Composition comprising interleukin-12 p40 and IL-B30 polypeptide or its  
 segment, useful for ameliorating rheumatoid arthritis, osteoarthritis,  
 PT atherosclerosis, multiple sclerosis, vasculitis and tumour -  
 XX  
 Disclosure; Page 11-12; 69pp; English.  
 XX  
 This sequence shows mouse interleukin-B30. Fragments of this protein  
 CC may be used in the composition of the invention. The composition  
 CC comprises a substantially pure polypeptide comprising a number of  
 CC distinct segments of at least 7 contiguous amino acids from IL-12 p40  
 CC and/or IL-B30, and a substantially pure polypeptide comprising a  
 CC segment of at least 11 contiguous amino acids from IL-12 p40 and/or  
 CC IL-B30. The composition is useful for modulating physiology or  
 CC development of a cell or tissue in a host organism, resulting in an  
 CC increased or decreased production of Interferon-gamma (IFNgamma), an  
 CC enhanced Th1 response such as anti-tumour effect, adjuvant effect,  
 CC anti-viral effect or antagonized allergic effect, and amelioration  
 CC of an autoimmune condition or a chronic inflammatory condition.  
 CC IL-B30 or its agonist is useful inducing the proliferation of memory  
 CC T-cells. An agonist or antagonist of IL-B30 protein is useful for  
 CC modulating the trafficking or activation of a leukocyte in an animal  
 CC experiencing science or symptoms of autoimmunity, an inflammatory  
 CC condition, tissue specific autoimmunity, degenerative autoimmunity,  
 CC rheumatoid arthritis, osteoarthritis, atherosclerosis, multiple  
 CC sclerosis, vasculitis, delayed hypersensitivities, skin grafting, a  
 CC transplant, spinal injury, stroke, neurodegeneration, an infectious  
 CC disease, ischaemia, cancer, tumour, multiple myeloma, Castleman's  
 CC disease, postmenopausal osteoporosis or IL-6-associated diseases.

CC IL-12 p40/IL-B30 is useful as an immunogen for the production a  
CC antisera or antibodies specific for binding.  
XX  
SQ Sequence 196 AA;  
Query Match 100.0%; Score 1038; DB 22; Length 196;  
Best Local Similarity 100.0%; Pred. No. 1.2e-99;  
Matches 196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60  
Db 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60  
Qy 61 EDEETKNNVPRIQCEGDCDPQGLKDNSQFCLOTRQGLAFYKHLSDIFKGEPAALLPDS 120  
Db 61 EDEETKNNVPRIQCEGDCDPQGLKDNSQFCLOTRQGLAFYKHLSDIFKGEPAALLPDS 120  
Qy 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQQWQRPRLRSKILRSLOAFIAIARV 180  
Db 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQQWQRPRLRSKILRSLOAFIAIARV 180  
Qy 181 FAHGAATLTPLVPTA 196  
Db 181 FAHGAATLTPLVPTA 196  
RESULT 5  
AAAY29783  
ID AAY29783 standard; Protein; 189 AA.  
AC AAY29783;  
XX  
DT 04-NOV-1999 (first entry)  
DE Human interleukin B30.  
XX  
KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW interleukin B30; DCRS1; DCRS1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /label= signal  
FT Protein 22..189  
FT /label= IL-B30  
XX  
PN WO9940195-A1.  
XX  
PD 12-AUG-1999.  
XX  
PF 05-FEB-1999; 99WO-US02600.  
XX  
PR 13-MAY-1998; 98US-0078194.  
PR 06-FEB-1998; 98US-0073941.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Kastelein RA, Mattson JD, McClanahan TK;  
XX  
DR WPI; 1999-527306/44.  
DR N-PSDB; AAZ08865.  
XX  
PT New receptor subunits useful in the treatment inflammatory disorders  
XX  
PS Claim 2; Page 26-27; 133pp; English.  
CC  
CC The 'present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit I (DCRS1) protein and DNAX soluble receptor  
CC subunit I (DCRS1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)

CC proteins, or DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DCRS1 and DCRS1 are useful as immunogens for generating  
CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the specifically claimed human IL-B30, for use in the  
CC composition of the present invention.  
XX  
SQ Sequence 189 AA;  
Query Match 69.2%; Score 718.5; DB 20; Length 189;  
Best Local Similarity 74.6%; Pred. No. 1.8e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps  
Qy 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60  
Db 1 MLDCAVIMLWLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 59  
Qy 61 EDEETKNNVPRIQCEGDCDPQGLKDNSQFCLOTRQGLAFYKHLSDIFKGEPAALLPDS 120  
Db 60 GDEETNDVPHIQCGDCDPQGLKDNSQFCLOTRQGLAFYKHLSDIFKGEPAALLPDS 119  
Qy 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSLSSSQQWQRPRLRSKILRSLOAFIAIARV 180  
Db 120 PVAQLHASLLGLSOLLQPEGHWHWETQIPSLSPSPQWQRLRLFRKILRSLOAFIAIARV 179  
Qy 181 FAHGAATLT 189  
Db 180 FAHGAATLS 188  
RESULT 6  
AAW95002  
ID AAW95002 standard; Protein; 189 AA.  
XX  
AC AAW95002;  
XX  
DT 21-MAY-1999 (first entry)  
DE Human interleukin-B30 (IL-B30) polypeptide.  
XX  
KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferatio  
KW inflammatory condition; drug screening; human.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..21  
FT /note= "signal peptide"  
FT Protein 22..189  
FT /note= "mature protein"  
XX  
PN WO9905280-A1.  
XX  
PD 04-FEB-1999.  
XX  
PF 24-JUL-1998; 98WO-US15423.  
XX  
PR 25-JUL-1997; 97US-0900905.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Bazan JF;  
XX  
DR WPI; 1999-142935/12.  
DR N-PSDB; AAX17786.



XX Newly isolated or recombinant polynucleotide encoding mammalian  
PT cytokine interleukin-B30 (IL-B30), including fragments - useful for  
PT regulating activation, development, differentiation and function of  
PT various cell types, and for diagnosing and treating conditions  
PT associated with IL-B30  
XX  
PS Claim 2; Page 8-9; 83pp; English.  
PS  
XX This represents a human cytokine interleukin-B30 (IL-B30) polypeptide.  
CC Host cells containing a vector comprising the IL-B30 nucleic acid are  
CC used for the recombinant production of the protein. The polynucleotides  
CC are useful for diagnosis of IL-B30 mediated conditions, and forensic  
CC science (e.g. to distinguish rodent from human, or as a marker to  
CC distinguish between different cells exhibiting differential expression or  
CC modification patterns). The IL-B30 (including fragments), together with  
CC antibodies that bind to IL-B30 are useful for teaching purposes. They  
CC are also used for treating conditions associated with abnormal physiology  
CC or development, including inflammatory conditions. The polypeptide  
CC cytokine should mediate cytokine synthesis and proliferation in cells.  
CC IL-B30 is useful for drug screening to identify compounds having binding  
CC affinity to IL-B30.  
XX  
SQ Sequence 189 AA;

Query Match 69.2%; Score 718.5; DB 20; Length 189;  
Best Local Similarity 74.6%; Pred. No. 1.8e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLCRAVIMLWLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMLLREE 60  
DB 1 MLGSRVAMLLLLPMTAQGRAVPGGSPAWTQCQQLSKLCTLAWSAHLVGHMD-LREE 59  
QY 61 EDEETKNVPRIQCEGDCPDGLKDNSQFCLOIRQGLAFYKHLSDIFKGEPAALLPS 120  
DB 60 GDEETNDVPHIQCGDCPDGLKDNSQFCLOIRHQGLIFYEKLGSDIFTGEPSELLPS 119  
QY 121 PMEQLHTSLGLSQQLOPEDHPRETQMPSSSQWQRPPLRSKILRSLOAFLAIAARV 180  
DB 120 PVAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSQPWQRLRLRPFKILRSLOAFVAVARV 179  
QY 181 FAHGAATLT 189  
DB 180 FAHGAATLS 188

RESULT 7  
AAB01981  
ID AAB01981 standard; Protein; 189 AA.  
AC AAB01981;  
XX  
XX 27-SEP-2000 (first entry)  
XX  
XX Human interleukin-B30 (IL-B30).  
XX  
XX Interleukin-B30; IL-B30; human; cytokine; cellular signalling;  
KW immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;  
KW granulocyte colony stimulating factor; immune disorder;  
KW inflammatory disease; autoimmune disease; antigen; antibody.  
XX  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..21  
FT /note= "Signal peptide"  
FT Protein 22..189  
FT /note= "Mature human IL-B30"  
XX  
XX US6060284-A.  
XX  
XX 09-MAY-2000.  
XX  
XX

PF 24-JUL-1998; 98US-0122443.  
XX  
PR 25-JUL-1997; 97US-0053765.  
XX  
PA (SCHE ) SCHERING CORP.  
XX  
PI Bazan JF;  
XX  
XX WPI; 2000-364420/31.  
DR N-PSDB; AAA52577.  
XX  
XX Novel recombinant DNA encoding cytokines especially interleukin-B30  
PT useful as probes or primers for diagnosing immune disorders including  
PT autoimmune or chronic inflammatory conditions  
PT  
XX  
XX Claim 1; Column 5-8; 32pp; English.  
XX  
XX This sequence represents human interleukin-B30 (IL-B30). IL-B30  
CC is a novel cytokine, exhibiting significant homology to IL-6 and  
CC GCSF (granulocyte colony stimulating factor). Cytokines play a critical  
CC role in signalling between immune or other cells during an immune  
CC response. The precise role of IL-B30 is not yet known - it is likely  
CC to have either a stimulatory or an inhibitory effect on haematopoietic cells  
CC such as T-cells, B-cells, natural killer (NK) cells and macrophages.  
CC Alternatively, it may affect vascular physiology or development, or have  
CC neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and  
CC antagonists are useful in the diagnosis and treatment of disorders  
CC associated with abnormal expression or activity of IL-B30 e.g.,  
CC inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are  
CC useful for recombinant expression of IL-B30 in a host cell, and as a  
CC source of probes and primers. The IL-B30 probes and primers can be used  
CC to detect levels of IL-B30 expression in samples from patients suspected  
CC of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may  
CC also be used to identify homologous genes in other species. IL-B30  
CC protein or its fragments are useful as antigens for raising antibodies to  
CC various linear and conformational epitopes. Such antibodies may be used  
CC to detect levels of IL-B30 protein in a sample.  
XX  
XX Sequence 189 AA;

Query Match 69.2%; Score 718.5; DB 21; Length 189;  
Best Local Similarity 74.6%; Pred. No. 1.8e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLCRAVIMLWLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHMLLREE 60  
DB 1 MLGSRVAMLLLLPMTAQGRAVPGGSPAWTQCQQLSKLCTLAWSAHLVGHMD-LREE 59  
QY 61 EDEETKNVPRIQCEGDCPDGLKDNSQFCLOIRQGLAFYKHLSDIFKGEPAALLPS 120  
DB 60 GDEETNDVPHIQCGDCPDGLKDNSQFCLOIRHQGLIFYEKLGSDIFTGEPSELLPS 119  
QY 121 PMEQLHTSLGLSQQLOPEDHPRETQMPSSSQWQRPPLRSKILRSLOAFLAIAARV 180  
DB 120 PVAQLHASLLGLSQQLOPEGHWHWTQIIPSLSPSQPWQRLRLRPFKILRSLOAFVAVARV 179  
QY 181 FAHGAATLT 189  
DB 180 FAHGAATLS 188

RESULT 8  
AAB47120  
ID AAB47120 standard; Protein; 189 AA.  
XX  
XX AAB47120;  
XX  
XX 04-JUN-2001 (first entry)  
XX  
XX Human IL-B30.  
XX  
XX Human; mouse; interleukin-B30; IL-12 p40; IL-B30; interferon-gamma;  
KW IFNgamma; Th1 response; autoimmune disease; chronic inflammation;



CC for treating, preventing or ameliorating medical conditions in humans  
 CC and animals. The polynucleotides can be used as markers for tissues in  
 CC which the protein is preferentially expressed, as molecular weight  
 CC markers on Southern gels, and as chromosome markers or tags to identify  
 CC chromosomes or to map gene positions. The proteins can be used in the  
 CC treatment of immune deficiencies and disorders, such as severe combined  
 CC immunodeficiency (SCID), as well as viral, bacterial, fungal and other  
 CC infections. These infections include human immunodeficiency virus (HIV),  
 CC hepatitis, herpesviruses, mycobacteria, Leishmania spp., malaria and  
 CC candidiasis. The proteins can be used to treat autoimmune disorders such  
 CC as connective tissue disease, multiple sclerosis, systemic lupus  
 CC erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation,  
 CC Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent  
 CC diabetes mellitus, myasthenia gravis, graft-versus-host-disease and  
 CC autoimmune inflammatory eye disease. The proteins can also be used to  
 CC treat allergic conditions, such as asthma. AAA16698 to AAA16774 represent  
 CC probes for the human secreted proteins from the present invention.  
 XX  
 SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;  
 Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLLPWTQGLAVPRSSPDWAOQQLSRNLCMLAWNAHAPAGHMNLLREE 60  
 DB 1 MLGSRVAMLLLLLPWTAQGRAVPGGSSPAWTQCQLSKLCTLAWSAHLVGHMD-LREE 59  
 QY 61 EDEETKNVPRIOCEDGCDPQGLKNSQFCQIRIQGLAFYKHLLDSDIFKGEPAALLPDS 120  
 DB 60 GDEETNDVPHIQCGDGDGCDPQGLRDNQFCQIRIQGLIFYEKLLGSDIFTGEPSSLPDS 119  
 QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQWOPRLRLSKILRSLOAFIAIARV 180  
 DB 120 PVQQLHASLLGLSOLLQPEGHWHETQOIPSLSPSPQWQRLRLRFLKILRSLOAFVAVARV 179  
 QY 181 FAHGAATLT 189  
 DB 180 FAHGAATLS 188

## RESULT 10

AA154606  
 ID AAY54606 standard; Protein; 189 AA.

XX  
 AC AAY54606;

XX  
 DT 01-FEB-2000 (first entry)

XX  
 DE SGRF protein sequence.

XX  
 KW SGRF; human; Interleukin-6 G-CSF related factor; cell proliferation;  
 KW immune system; haematopoietic system; therapy.

XX  
 OS Homo sapiens.

XX  
 PN WO954357-A1.

XX  
 PD 28-OCT-1999.

XX  
 PF 14-APR-1999; 99WO-JP01997.

XX  
 PR 14-APR-1998; 98JP-0121805.

XX  
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX  
 PI Hirata Y;

XX  
 DR WPI: 2000-013230/01.

XX  
 DR N-PSDB; AA237262, AA237263.

XX  
 PT Novel cytokine-like protein, with activity of supporting proliferation  
 PT of myeloid cells, useful in treating abnormality of cell proliferation

PT In immune and haematopoiesis systems -  
 XX  
 PS Claim 1: Fig 1; 69pp; Japanese.  
 XX  
 CC This sequence is the Interleukin-6 G-CSF related factor (SGRF)  
 CC protein of the invention. The protein is a member of the IL-6/G-CSF/MSF  
 CC family. The protein can be used in drugs for treating diseases due to  
 CC abnormality of cell proliferation in the immune system and haematopoietic  
 CC system.

XX  
 SQ Sequence 189 AA;

Query Match 69.1%; Score 717.5; DB 21; Length 189;  
 Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
 Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MLDCAVIMLLPWTQGLAVPRSSPDWAOQQLSRNLCMLAWNAHAPAGHMNLLREE 60  
 DB 1 MLGSRVAMLLLLLPWTAQGRAVPGGSSPAWTQCQLSKLCTLAWSAHLVGHMD-LREE 59  
 QY 61 EDEETKNVPRIOCEDGCDPQGLKNSQFCQIRIQGLAFYKHLLDSDIFKGEPAALLPDS 120  
 DB 60 GDEETNDVPHIQCGDGDGCDPQGLRDNQFCQIRIQGLIFYEKLLGSDIFTGEPSSLPDS 119  
 QY 121 PMEQLHTSLGLSOLLQPEDHPRETQOMPSSSSQWOPRLRLSKILRSLOAFIAIARV 180  
 DB 120 PVQQLHASLLGLSOLLQPEGHWHETQOIPSLSPSPQWQRLRLRFLKILRSLOAFVAVARV 179  
 QY 181 FAHGAATLT 189  
 DB 180 FAHGAATLS 188

## RESULT 11

AAU12287  
 ID AAU12287 standard; Protein; 189 AA.

XX  
 AC AAU12287;

XX  
 DT 24-OCT-2001 (first entry)

XX  
 DE Human PRO5798 polypeptide sequence.

XX  
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
 KW adipocyte; A-peptide; factor VIIA; gene therapy.

XX  
 OS Homo sapiens.

XX  
 PN WO200140466-A2.

XX  
 PD 07-JUN-2001.

XX  
 PF 01-DEC-2000; 2000WO-US32678.

XX  
 PR 01-DEC-1999; 99WO-US28301.

XX  
 PR 01-DEC-1999; 99WO-US28634.

XX  
 PR 02-DEC-1999; 99WO-US28551.

XX  
 PR 02-DEC-1999; 99WO-US28564.

XX  
 PR 02-DEC-1999; 99WO-US28565.

XX  
 PR 09-DEC-1999; 99US-0170262.

XX  
 PR 16-DEC-1999; 99WO-US30095.

XX  
 PR 20-DEC-1999; 99WO-US30911.

XX  
 PR 20-DEC-1999; 99WO-US30999.

XX  
 PR 30-DEC-1999; 99WO-US31243.

XX  
 PR 06-JAN-2000; 2000WO-US00277.

XX  
 PR 06-JAN-2000; 2000WO-US00376.

XX  
 PR 11-FEB-2000; 2000WO-US03565.

XX  
 PR 18-FEB-2000; 2000WO-US04341.

XX  
 PR 18-FEB-2000; 2000WO-US04342.

XX  
 PR 22-FEB-2000; 2000WO-US04414.

XX  
 PR 24-FEB-2000; 2000WO-US04914.

PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 10-NOV-2000; 2000WO-US30873.  
PR (GETH ) GENENTECH INC.  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI: 2001-408281/43.  
DR N-PSDB; AAS21359.  
XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing  
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
PT lung, breast, prostate, cervical -  
XX Claim 12; Fig 232; 813pp; English.  
PS  
XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
CC PRO polypeptides. The PRO polypeptides are useful to detect other  
CC PRO polypeptides, to link bioactive molecules to cells expressing  
CC PRO polypeptides, to modulate biological activities of cells expressing  
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample.  
CC Some of the 275 sequences are also useful to stimulate the release of  
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
CC proliferation or differentiation of chondrocytes, the proliferation or  
CC gene expression in pericyte cells, the release of proteoglycans from  
CC cartilage, the proliferation of inner ear utricular supporting cells or  
CC of T-lymphocytes, the release of a cytokine from peripheral blood  
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
CC to factor VIITA. The PRO polypeptides can be used in assays to identify  
CC molecules involved in binding interactions. The polynucleotides encoding  
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy.  
XX  
XX Sequence 189 AA:  
Query Match 69.1%; Score 717.5; DB 22; Length 189;  
Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLDCRAVIMLLPWTQGLAVPRSSPDWACQQLSRNLCMLAWNAHAPAGHNNLREE 60  
Db 1 MLGSRAVMLLLPWTQGRAVPGGSSPAWTQCQQLSQKLCCTLAWSAHLVGHMD-LREE 59  
QY 61 EDEETKNNVPRQCEDGCDPQGLKDNQSFCLQRIQGLAFYKHLLDSDIFKGEPAALLPDS 120  
Db 60 GDEETNDVPHIQCGDGPQGLRDNQSFCLQRIHQGLDIFYEKLLGSDIFTFGEPSLLPDS 119  
QY 121 PMEQLHTSLGLSQQLQDHPHRETQMPSLSSSQOQWRLLRSKLRSQAFAIAARV 180  
Db 120 PVGQLHASLLGLSQQLQDHPHRETQMPSLSPSPQWQRLRLFRKLRSQAFAVAARV 179  
QY 181 FAHGAATLT 189  
Db 180 FAHGAATLS 188  
RESULT 12  
AAB48070

ID AAB48070 standard; protein; 189 AA.  
XX AAB48070;  
AC  
XX 19-MAR-2001 (first entry)  
DT  
XX Human extracellular signaling molecule (EXCS) (ID 2933038CD1).  
DE  
XX Extracellular signaling molecule; EXCS: anti-inflammatory; human;  
KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;  
KW viricide; antibacterial; anti-HIV; human immunodeficiency virus;  
KW antinfertility; cerebroprotective; nootropic; antitumor; antifungal;  
KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;  
KW keratolytic; protozoacide; gene therapy.  
XX Homo sapiens.  
OS  
XX WO200070049-A2.  
PN  
XX 23-NOV-2000.  
PD  
XX 19-MAY-2000; 2000WO-US13975.  
PF  
XX 19-MAY-1999; 99US-0134949.  
PR 15-JUL-1999; 99US-0144270.  
PR 30-JUL-1999; 99US-0146700.  
PR 04-OCT-1999; 99US-0157508.  
XX (INCY-) INCYTE GENOMICS INC.  
PA  
XX Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;  
PI Azimzai Y, Lu DAM, Patterson C;  
PI  
XX WPI: 2001-025021/03.  
DR N-PSDB; AAC84306.  
XX New human extracellular signaling nucleic acids and polypeptides useful  
PT for diagnosing, treating and preventing infections and  
PT gastrointestinal, neurological, reproductive, and  
PT autoimmune/inflammatory disorders -  
XX Claim 1; Page 92; 114pp; English.  
XX The invention provides human extracellular signaling molecules (EXCS)  
CC and polynucleotides which identify and encode EXCS. EXCS can be  
CC expressed by standard recombinant methodology. The amino acid and nucleic  
CC acid sequences of EXCS are useful for diagnosing, treating and  
CC preventing infections and gastrointestinal (peptic ulcer, dysphagia,  
CC pancreatitis), neurological (e.g. epilepsy, ischemic cerebrovascular  
CC disease, stroke), reproductive (infertility, ovulatory defects,  
CC endometriosis), autoimmune /inflammatory (actinic keratosis, acquired  
CC immunodeficiency syndrome (AIDS), Addison's disease), and cell  
CC proliferative disorders including cancers (of the breast, adrenal gland,  
CC bone). They may also be used to treat fatal familial insomnia,  
CC nutritional and metabolic diseases of the nervous system, myopathies,  
CC mental disorders (anxiety, schizophrenia, mood), as well as infections  
CC caused by parasites (malaria, leishmania, trypanosoma), viral  
CC (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus,  
CC staphylococcus, bacillus), and fungal (aspergillus, blastomycosis,  
CC dermatophytes) agents. The nucleic acids, polypeptides, antagonists,  
CC agonists, pharmaceutical compositions, and antibodies may also be used  
CC for treating or preventing disorders associated with increased or  
CC decreased expression or activity of EXCS. EXCS polynucleotides may also  
CC be used to detect and quantify gene expression in biopsied tissues in  
CC which expression of EXCS may be correlated with the disease, to determine  
CC presence or excess expression of EXCS, to monitor regulation of EXCS  
CC levels during therapeutic intervention, to detect the presence of  
CC associated disorders, as targets in microarray, to generate hybridization  
CC probes, and to detect differences in gene sequences among normal, carrier  
CC or affected individuals. Antibodies may also be used in diagnosing  
CC disorders, in monitoring patients being treated with EXCS agonists,  
CC antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS  
CC of the invention.

XX SQ Sequence 189 AA;  
Query Match 69.1%; Score 717.5; DB 22; Length 189;  
Best Local Similarity 74.6%; Pred. No. 2.3e-66;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLDCAVIMLLPWVTOGLAVPRSSPDWAQCOQLSRNLCMLAWNAHAPAGHMNLLREE 60  
II III:II III II III III:II III:II III:II III:II III:II  
DB 1 MGSRAVMLLLPWTAGRAVPGSSPAWTQCQQLSQKLTCTLAWSAHPVLVGHMD-LREE 59  
QY 61 EDEETKNVPRIQCDGCDPGLKNDNQFCLQRTQGLAYKHLSDSDIFKGPALLPDS 120  
III:II III:II III:II III:II III:II III:II III:II III:II III:II  
DB 60 GDEETNDVPHIQDGDGDPQGLRDNQFCLQRTQGLAYKHLSDSDIFKGPALLPDS 119  
QY 121 PNEQLHTSLGLSQLQLOPDHPRTEQPMPSLSSSQWQRPRLKRLKILRSLOAFATAARV 180  
II III:II III:II III:II III:II III:II III:II III:II III:II  
DB 120 PVGQLHASLGLSQLQLOPDHPRTEQPMPSLSSSQWQRPRLKRLKILRSLOAFATAARV 179  
QY 181 FAHGAATLT 189  
II III:II III:II III:II III:II III:II III:II III:II III:II  
DB 180 FAHGAATLT 188  
RESULT 13  
AAY29787  
ID AAY29787 standard; Protein; 102 AA.  
XX AC AAY29787;  
XX DE Partial pig interleukin B30 protein.  
XX KW DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;  
KW interleukin B30; DSRs1; DCRs1; IL-B30; cytokine receptor; diagnosis;  
KW inflammatory disorder; inflammatory response; innate immunity;  
KW morphogenic development; immunological disorder.  
XX OS Sus scrofa.  
XX PN WO9940195-A1.  
XX PD 12-AUG-1999.  
XX PF 05-FEB-1999; 99WO-US02600.  
XX PR 13-MAY-1998; 98US-0078194.  
XX PR 06-FEB-1998; 98US-0073941.  
XX PA (SCHE ) SCHERING CORP.  
XX PI Kasteleijn RA, Mattson JD, McClanahan TK;  
XX WPI; 1999-527306/44.  
XX PT New receptor subunits useful in the treatment inflammatory disorders  
XX PS Disclosure; Page 29; 133pp; English.  
XX CC The present invention describes a composition (I) comprising DNAX  
CC cytokine receptor subunit 1 (DCRS1) protein and DNAX soluble receptor  
CC subunit 1 (DSRS1) protein, which together encode a new mammalian  
CC cytokine-related receptor (R), or DCRs1 and interleukin B30 (IL-B30)  
CC proteins, or DSRs1 and IL-B30 proteins. (I) comprising DSRs1 and DCRs1  
CC is useful for screening for ligands (i.e. agonists/antagonists) from  
CC a library of compounds, which are useful for modulating the physiology  
CC or development of a cell or tissue culture e.g. inflammatory responses,  
CC innate immunity and/or morphogenic development. (R), antibodies and  
CC ligands are useful for treatment of conditions, especially immunological  
CC disorders, associated with conditions exhibiting abnormal expression of  
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates,  
CC and the subunits DSRs1 and DCRs1 are useful as immunogens for generating

CC antibodies, or as antigens for binding antibodies. Nucleic acids  
CC encoding (R) are useful for identifying related DNAs and mRNAs, and  
CC variants from other individuals or species. The present sequence  
CC represents the partial pig IL-B30, given in the present invention.  
XX SQ Sequence 102 AA;  
Query Match 34.3%; Score 356; DB 20; Length 102;  
Best Local Similarity 72.3%; Pred. No. 3.8e-29;  
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps 0;  
QY 90 CLQRIHQGLAYKHLSDSDIFKGPALLPSPMEQLHTSLGLSQLQLOPDHPRTEQOMP 149  
II III:II III:II III:II III:II III:II III:II III:II III:II  
DB 2 CLQRIHQGLVPEYKLLGSDIFTGPELHPDGSVQLHSLGLRQLQLOPDHPRTEQOMP 61  
QY 150 SILSSSQWQRPRLKRLKILRSLOAFATAARVFAHGAATLT 190  
II III:II III:II III:II III:II III:II III:II III:II III:II  
DB 62 SPSPSQWQRPRLKRLKILRSLOAFATAARVFAHGAATLT 102  
RESULT 14  
AAW95004  
ID AAW95004 standard; peptide; 102 AA.  
XX AC AAW95004;  
XX DT 21-MAY-1999 (first entry)  
XX DE Pig interleukin-B30 (IL-B30) polypeptide.  
XX KW Cytokine; interleukin-B30; IL-B30; forensic science; cell proliferation;  
KW inflammatory condition; drug screening; pig.  
XX OS Sus scrofa.  
XX PN WO9905280-A1.  
XX PD 04-FEB-1999.  
XX PF 24-JUL-1998; 98WO-US15423.  
XX PR 25-JUL-1997; 97US-0900905.  
XX PA (SCHE ) SCHERING CORP.  
XX PI Bazan JF;  
XX WPI; 1999-142935/12.  
XX PT Newly isolated or recombinant polynucleotide encoding mammalian  
PT cytokine interleukin-B30 (IL-B30), including fragments useful for  
PT regulating activation, development, differentiation and function of  
PT various cell types, and for diagnosing and treating conditions  
PT associated with IL-B30  
XX PS Claim 1; Page 11-12; 83pp; English.  
XX CC This invention relates to mammalian cytokine interleukin-B30 (IL-B30)  
CC polypeptides. Host cells containing a vector comprising the IL-B30  
CC nucleic acids are used for the recombinant production of the proteins.  
CC The polynucleotides are useful for diagnosis of IL-B30 mediated  
CC conditions, and forensic science (e.g. to distinguish rodent from human,  
CC or as a marker to distinguish between different cells exhibiting  
CC differential expression or modification patterns). The IL-B30 (including  
CC fragments), together with antibodies that bind to IL-B30 are useful for  
CC teaching purposes. They are also used for treating conditions associated  
CC with abnormal physiology or development, including inflammatory  
CC conditions. The polypeptide cytokine should mediate cytokine synthesis  
CC and proliferation in cells. IL-B30 is useful for drug screening to  
CC identify compounds having binding affinity to IL-B30. The present  
XX sequence represents a pig IL-B30.  
XX SQ Sequence 102 AA;

Query Match 34.3%; Score 356; DB 20; Length 102;  
Best Local Similarity 72.3%; Pred. NO. 3.8e-29;  
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

[illegible]

RESULT 15	
AA01983	
ID	AA01983 standard; Protein; 102 AA.
XX	
AC	AA01983;
XX	
DT	27-SEP-2000 (first entry)
XX	
DE	Mature porcine interleukin-B30 (IL-B30).
XX	
KW	Interleukin-B30; IL-B30; porcine; pig; cytokine; cellular signalling;
KW	immune response; haematopoietic cell; IL-6 homologue; GCSF homologue;
KW	granulocyte colony stimulating factor; immune disorder;
XX	inflammatory disease; autoimmune disease; antigen; antibody.
XX	
OS	Sus scrofa.
XX	
PN	US6060284 -A.
XX	
PD	09-MAY-2000.
XX	
PF	24-JUL-1998; 98US-0122443.
XX	
PR	25-JUL-1997; 97US-0053765.
XX	
PA	(SCHE ) SCHERING CORP.
XX	
PI	Bazan JF;
XX	
DR	WPI; 2000-364420/31.
XX	
PT	Novel recombinant DNA encoding cytokines especially interleukin-B30
PT	useful as probes or primers for diagnosing immune disorders including
PT	autoimmune or chronic inflammatory conditions -
XX	
PS	Claim 1: Column 45-46: 32bp: English.

This sequence represents porcine interleukin-B30 (IL-B30). IL-B30 is a novel cytokine, exhibiting significant homology to IL-6 and GCSF (granulocyte colony stimulating factor). Cytokines play a critical role in signalling between immune or other cells during an immune response. The precise role if IL-B30 is not yet known - it is likely to have either a stimulatory or an inhibitory effect on haematopoietic cells such as T-cells, B-cells, natural killer (NK) cells and macrophages. Alternatively, it may affect vascular physiology or development, or have neuronal effects. IL-B30, its fragments, IL-B30 nucleotides, agonists and antagonists are useful in the diagnosis and treatment of disorders associated with abnormal expression or activity of IL-B30 e.g., inflammatory or autoimmune disorders. Nucleotides encoding IL-B30 are useful for recombinant expression of IL-B30 in a host cell, and as a source of probes and primers. The IL-B30 probes and primers can be used to detect levels of IL-B30 expression in samples from patients suspected of having an inflammatory or autoimmune disorder. IL-B30 nucleotides may also be used to identify homologous genes in other species. IL-B30 protein or its fragments are useful as antigens for raising antibodies to various linear and conformational epitopes. Such antibodies may be used to detect levels of IL-B30 protein in a sample.

Sequence<sup>a</sup> 102 AA;

Search completed: November 20, 2002, 11:53:01  
Job time : 35.6 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:54:30 : Search time 7.63636 Seconds  
(without alignments)  
401.978 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLCRAVIMLWLLPWVTOGL.....AARVFAHGAATLEPLVPIA 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/us08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/FCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/FCTUS\_PUBCOMB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	88	8.5	181 10	US-09-764-864-1144
2	88	8.5	181 10	US-09-764-864-1144
3	84	8.1	212 10	US-09-854-280-14
4	84	8.1	212 10	US-09-854-280-14
5	81.5	7.9	175 10	US-09-754-532-80
6	79.5	7.7	175 10	US-09-754-532-79
7	78.5	7.6	175 10	US-09-754-532-92
8	78.5	7.6	175 10	US-09-754-532-106
9	78.5	7.6	175 10	US-09-754-532-109
10	78	7.5	285 10	US-09-815-242-5068
11	77.5	7.5	348 12	US-10-003-496-6
12	76.5	7.4	174 10	US-09-760-008A-1
13	76.5	7.4	174 10	US-09-950-473-2
14	76.5	7.4	174 12	US-10-016-403-1
15	76.5	7.4	174 12	US-10-016-403-2
16	76.5	7.4	174 12	US-10-016-403-3
17	76.5	7.4	174 12	US-10-003-496-1
18	76.5	7.4	175 10	US-09-754-532-2
19	76.5	7.4	175 10	US-09-754-532-67

ALIGNMENTS

RESULT 1

US-09-764-864-1144

; Sequence 1144, Application US/09764864

; Patent No. US20020132753A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PT223

; CURRENT APPLICATION NUMBER: US/09/764.864

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1792

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1144

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-764-864-1144

Query Match 8.5%; Score 88; DB 10; Length 181;

Best Local Similarity 23.7%; Pred. No. 0.057;

Matches 47; Conservative 19; Mismatches 50; Indels 82; Gaps 11;

Qy	11	WLLPWVTOGLAVPRSSP-----DWAQCQOLSRNLCMLAWNAHA-PAGHMNLLREEDDEET	65
Db	8	WLLPKPSSICLPGTWAPPGSSHWVACGL-----WGPGAGPA-----	45
Qy	66	KNNVPRIQCEDGCDPOGLKDNQSCFLQRIROGL-----AFYKHLIDS-DIF	110
Db	46	-----TGSPQWVGKE-----RRARLGCFFPHSPWTLREELSWANGCHVSQDGMV	89
Qy	111	KGEAL-----LPDPSPEQLHTSLGLSQLLOPDHPRETQOMPSLSSSQOWRP-----	160
Db	90	GCHRSVAGYWEFFLSFSLSLHPFSGMCL-----PR--SRSPSPSPQWKKPVIDTA	139
Qy	161	-----LLRSKILRSLOAFL 174	
Db	140	VGGRCKSLIFGALEGL 157	

RESULT 2

US-09-764-864-1559

; Sequence 1559, Application US/09764864  
; Patent No. US20020132753A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PT223

; CURRENT APPLICATION NUMBER: US/09/764,864

; PRIOR FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 1792

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1559

; LENGTH: 181

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-764-864-1559

Query Match 8.5%; Score 88; DB 10; Length 181;

Best Local Similarity 23.7%; Pred. No. 0.057; 50; Indels 82; Gaps 11;

Matches 47; Conservative 19; Mismatches 50; Indels 82; Gaps 11;

QY 11 WLLPWVTQGLAVPRSSP-----DWAQCQQLSRNLCMLAWNAHA-PAGHMNLLREEDEET 65

Db 8 WLLPPKPSGICLCTWAPGSSHWACGL-----WPGAGPA----- 45

QY 66 KNNVPTQCEGCDPQGLKDNSQFCQIRQGL-----APYKHLDS-DIF 110

Db 46 -----TGSQPGWCKE-----RRARLGCFFHSPWTLREELSWANGCHVSDSDVM 89

QY 111 KGPAL-----LPDSPMEQLHTSLGLSOLLQPEDHPRETQMPSSSSQOQRP----- 160

Db 90 GGHRSVAGYWEFFLSLUSLHPSMGCL-----PR--SRSPSPSPQOMKKPVDTA 139

QY 161 -----LRSKILRSIQAPL 174

Db 140 VGGRLCKSLTFGALEGFL 157

RESULT 3

US-09-854-280-14

; Sequence 14, Application US/09854280

; Patent No. US20020052027A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Hanzhong

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF

; FILE REFERENCE: P1381R1C2

; CURRENT APPLICATION NUMBER: US/09/854,280

; PRIOR FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: US 09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/085,579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 60/113,621

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 26

; SEQ ID NO 14

; LENGTH: 212

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-280-14

Query Match 8.1%; Score 84; DB 10; Length 212;

Best Local Similarity 21.5%; Pred. No. 0.19;

Matches 38; Conservative 28; Mismatches 71; Indels 40; Gaps 7;

QY 15 WVTQGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREEDEETKNNVPRIQC 74

Db 59 YILDGIALRKET-----CNK--SNMCESKEALA-----ENNLPKMAE 97

RESULT 5

US-09-754-532-80

; Sequence 80, Application US/09754532

; Patent No. US20010016191A1

; GENERAL INFORMATION:

; APPLICANT: Osslund, Timothy D.

; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS

; NUMBER OF SEQUENCES: 110

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: Amgen Center, 1840 DeHavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: United States of America

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

QY 75 EDGCDPQGLKDNSQFCQIRQGLAFYKHLDD--SDIFKGPALLPDSPMEQLHTSLGL 132

Db 98 KDGCFQSGF--NEETCLVKIITGLLEFEVYLEYLQNRFESS-----EEQARAVQMSTKVL 150

QY 133 SOLLOPE-----DHPRETQMPSSSSQOQRPRLRSKILRSIQAFLAIAAR 179

Db 151 IOFLQKAKNLDATITPDPTTNASLLTKLQANQWLODMTTHILRSFKFLOSSLR 207

RESULT 4

US-09-854-208-14

; Sequence 14, Application US/09854208

; Patent No. US20020106743A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Jian

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Li, Hanzhong

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: P1381-R1

; CURRENT APPLICATION NUMBER: US/09/854,208

; CURRENT FILING DATE: 2001-05-10

; PRIOR APPLICATION NUMBER: US/09/311,832

; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: US 60/085,579

; PRIOR FILING DATE: 1998-05-15

; PRIOR APPLICATION NUMBER: US 60/113,621

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 26

; SEQ ID NO 14

; LENGTH: 212

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-854-208-14

Query Match 8.1%; Score 84; DB 10; Length 212;

Best Local Similarity 21.5%; Pred. No. 0.19;

Matches 38; Conservative 28; Mismatches 71; Indels 40; Gaps 7;

QY 15 WVTQGLAVPRSSPDWAQCQQLSRNLCMLAWNAHAPAGHMNLLREEDEETKNNVPRIQC 74

Db 59 YILDGIALRKET-----CNK--SNMCESKEALA-----ENNLPKMAE 97

QY 75 EDGCDPQGLKDNSQFCQIRQGLAFYKHLDD--SDIFKGPALLPDSPMEQLHTSLGL 132

Db 98 KDGCFQSGF--NEETCLVKIITGLLEFEVYLEYLQNRFESS-----EEQARAVQMSTKVL 150

QY 133 SOLLOPE-----DHPRETQMPSSSSQOQRPRLRSKILRSIQAFLAIAAR 179

Db 151 IOFLQKAKNLDATITPDPTTNASLLTKLQANQWLODMTTHILRSFKFLOSSLR 207

RESULT 5

US-09-754-532-80

; Sequence 80, Application US/09754532

; Patent No. US20010016191A1

; GENERAL INFORMATION:

; APPLICANT: Osslund, Timothy D.

; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS

; NUMBER OF SEQUENCES: 110

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: Amgen Center, 1840 DeHavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: United States of America

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk



```
;
;
; *COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-80
```

```
Query Match 7.9%; Score 81.5; DB 10; Length 175;
Best Local Similarity 30.4%; Pred. No. 0.26;
Matches 35; Conservative 17; Mismatches 36; Indels 27; Gaps 7;

QY 90 CLQRIROGLAFYKHLSDIFKG--EPALLPDSMPQQLHTS-----LLGLSOLLQ 137
||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 75 CLSQLHSLGLFYQGLLQA--LEGISPELGPTLDTLQLDVADFATTIWOQMEELGMAPALQ 132

QY 138 PEDHPRETQ--OMPSLSSSQOQRPRLRSKILRSLOAFIAIARVFAHGAATLTP 191
| ||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 133 P-----TQGAMPAPASA--FQRAGGVLVASHLQSFLEVSRYRLAH----LAQP 175
```

```
RESULT 6
US-09-754-532-79
; Sequence 79, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
```

```
;
;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-79
```

```
Query Match 7.7%; Score 79.5; DB 10; Length 175;
Best Local Similarity 30.9%; Pred. No. 0.42;
Matches 34; Conservative 16; Mismatches 37; Indels 23; Gaps 6;

QY 90 CLQRIROGLAFYKHLSDIFKG--EPALLPDSMPQQLHTS-----LLGLSOLLQ 137
||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 75 CLSQLHSLGLFYQGLLQA--LEGISPELGPTLDTLQLDVADFATTIWOQMEELGMAPALQ 132

QY 138 PEDHPRETQ--OMPSLSSSQOQRPRLRSKILRSLOAFIAIARVFAHGAATLTP 186
| ||::||::||::||::||::||::||::||::||::||::||::||::||
Db 133 P-----TQGAMPAPASA--FQRAGGVLVASHLQSFLEVSRYRLHAA 174
```

```
RESULT 7
US-09-754-532-92
; Sequence 92, Application US/09754532
; Patent No. US20010016191A1
; GENERAL INFORMATION:
; APPLICANT: Osslund, Timothy D.
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Angen Inc.
; STREET: Angen Center, 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States of America
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/754,532
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/448,716
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pessin, Karol
; REGISTRATION NUMBER: 34,899
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 805/499-5725
; TELEFAX: 805/499-8011
; INFORMATION FOR SEQ ID NO: 92:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-754-532-92
```

```
Query Match 7.6%; Score 78.5; DB 10; Length 175;
Best Local Similarity 30.4%; Pred. No. 0.54;
Matches 35; Conservative 16; Mismatches 37; Indels 27; Gaps 7;

QY 90 CLQRIROGLAFYKHLSDIFKG--EPALLPDSMPQQLHTS-----LLGLSOLLQ 137
||::||::||::||::||::||::||::||::||::||::||::||::||
Db 75 CLSQLHSLGLFYQGLLQA--LEGISPELGPTLDTLQLDVADFATTIWOQMEELGMAPALQ 132

QY 138 PEDHPRETQ--OMPSLSSSQOQRPRLRSKILRSLOAFIAIARVFAHGAATLTP 191
| ||::||::||::||::||::||::||::||::||::||::||::||
Db 133 P-----TQGAMPAPASA--FQRAGGVLVASHLQSFLEVSRYRLRH----LAQP 175

RESULT 8
```

wed Nov 20 13:29:04 2002

US-09-754-532-106  
; Sequence 106, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Osslund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Angen Inc.  
; STREET: Angen Center, 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/754,532  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION NUMBER: 08/448,716  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol  
; REGISTRATION NUMBER: 34,899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/499-5725  
; TELEFAX: 805/499-8011  
; INFORMATION FOR SEQ ID NO: 106:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-754-532-106

Query Match 7.6%; Score 78.5; DB 10; Length 175;  
Best Local Similarity 29.6%; Pred. No. 0.54;  
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;  
  
QY 90 CLQIRQGLAFYKHLSDIFKQ-EPALLPDSMPMEQLHTSL-----LGLSOLLQ 137  
||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 75 CLSQHSLGLFYQGLLQA--LEGISPGLPTLDTLQLDVAFATTIWQMEELGMAPALQ 132  
  
QY 138 PEDHPRETQ-QMPSLSSSQOQRPLRSKILRSLOAFIAARVFAHGAATLTPE 191  
| || ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 133 P-----TQGAMPAFASA--FORRAGGVLVASHLQSFLEVSRYRLRH----LAQP 175  
  
RESULT 9  
US-09-754-532-109  
; Sequence 109, Application US/09754532  
; Patent No. US20010016191A1  
; GENERAL INFORMATION:  
; APPLICANT: Osslund, Timothy D.  
; TITLE OF INVENTION: G-CSF ANALOG COMPOSITIONS AND METHODS  
; NUMBER OF SEQUENCES: 110  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Angen Inc.  
; STREET: Angen Center, 1840 DeHavilland Drive  
; CITY: Thousand Oaks  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/754,532  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA: 08/448,716  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pessin, Karol  
; REGISTRATION NUMBER: 34,899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 805/499-5725  
; TELEFAX: 805/499-8011  
; INFORMATION FOR SEQ ID NO: 109:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-754-532-109  
  
Query Match 7.6%; Score 78.5; DB 10; Length 175;  
Best Local Similarity 29.6%; Pred. No. 0.54;  
Matches 34; Conservative 17; Mismatches 37; Indels 27; Gaps 7;  
  
QY 90 CLQIRQGLAFYKHLSDIFKQ-EPALLPDSMPMEQLHTS-----LGLSOLLQ 137  
||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 75 CLSQHSLGLFYQGLLQA--LEGISPGLPTLDTLQLDVAFATTIWQMEELGMAPALQ 132  
  
QY 138 PEDHPRETQ-QMPSLSSSQOQRPLRSKILRSLOAFIAARVFAHGAATLTPE 191  
| || || ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DB 133 P-----TQGAMPAFASA--FORRAGGVLVASHLQSFLEVSRYRLRH----LAQP 175  
  
RESULT 10  
US-09-815-242-5068  
; Sequence 5068, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 14110  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5068  
; LENGTH: 285  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-5068





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 20, 2002, 11:53:05 ; Search time 12.2182 Seconds  
(without alignments)  
471.993 Million cell updates/sec

Title: US-09-658-699-4  
Perfect score: 1038  
Sequence: 1 MLDGRAVIMLLPWVTOGL.....AARVFAHGAATLPELVPVTA 196

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_A1:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1038	100.0	196	3	US-09-122-443-4
2	718.5	69.2	189	3	US-09-122-443-2
3	356	34.3	102	3	US-09-122-443-5
4	112	10.8	162	4	US-09-499-148-5
5	112	10.8	184	3	US-09-122-443-13
6	104	10.0	162	4	US-09-499-148-2
7	103	9.9	166	4	US-09-499-148-3
8	100	9.6	166	4	US-09-499-148-9
9	96	9.2	166	4	US-09-499-148-7
10	96	9.2	188	3	US-09-122-443-14
11	96	9.2	211	4	US-08-097-869-8
12	92.5	8.9	186	1	US-08-209-182C-6
13	92.5	8.9	186	5	PCT-US92-05612-6
14	91	8.8	166	4	US-09-499-148-6
15	89	8.6	212	4	US-09-487-792-14
16	88	8.5	184	2	US-08-693-182-2
17	88	8.5	184	2	US-09-008-482-2
18	88	8.5	185	1	US-07-918-181A-4
19	88	8.5	185	1	US-08-231-575-4
20	88	8.5	185	5	PCT-US93-06928-4
21	87.5	8.4	162	2	US-08-716-317-10
22	87.5	8.4	163	2	US-08-716-317-15
23	86.5	8.3	174	3	US-09-122-443-7
24	86.5	8.3	319	5	PCT-US94-04208-2
25	86.5	8.3	337	3	US-08-469-318-148
26	86.5	8.3	337	3	US-08-468-609A-148
27	86.5	8.3	337	4	US-08-446-872A-148

28	86.5	8.3	337	4	US-08-762-227A-148	Sequence 148, App
29	86.5	8.3	337	5	PCT-US95-01185-148	Sequence 148, App
30	86	8.3	185	1	US-07-918-181A-8	Sequence 8, Appli
31	86	8.3	185	1	US-08-231-575-8	Sequence 8, Appli
32	86	8.3	185	5	PCT-US93-06928-8	Sequence 8, Appli
33	84.5	8.1	185	5	PCT-US92-05612-2	Sequence 2, Appli
34	84.5	8.1	186	1	US-08-209-182C-2	Sequence 2, Appli
35	84	8.1	164	4	US-08-318-193-60	Sequence 60, Appl
36	84	8.1	166	4	US-09-499-148-1	Sequence 1, Appli
37	84	8.1	183	1	US-08-009-973-1	Sequence 1, Appli
38	84	8.1	184	1	US-08-567-047-2	Sequence 2, Appli
39	84	8.1	184	2	US-08-567-048-2	Sequence 2, Appli
40	84	8.1	184	6	5186931-1	Patent No. 5186931
41	84	8.1	185	1	US-07-632-070B-1	Sequence 1, Appli
42	84	8.1	185	1	US-07-918-181A-2	Sequence 2, Appli
43	84	8.1	185	1	US-08-231-575-2	Sequence 2, Appli
44	84	8.1	185	1	US-08-246-427A-5	Sequence 5, Appli
45	84	8.1	185	2	US-08-716-317-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-122-443-4  
; Sequence 4, Application US/09122443  
; Patent No. 6060284  
; GENERAL INFORMATION:  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/122,443  
; FILING DATE: 24-JUL-1998  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/053,765  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0758K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 196 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-122-443-4

Query Match	100.0%	Score 1038;	DB 3;	Length 196;
Best Local Similarity	100.0%;	Pred. No. 2.1e-109;		
Matches 196;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLDCRAVIMLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMAWNAHAPAGHNNLLREE	60	
DB	1	MLDCRAVIMLLPWVTOGLAVPRSSPDWAQCQQLSRNLCMAWNAHAPAGHNNLLREE	60	

QY 61 EDEETKNNVPRIOCGDCDQGLKDNQSCQLQRIQGLAFYKHLSDIFKGEPAALLPDS 120  
|||||  
Db 61 EDEETKNNVPRIOCGDCDQGLKDNQSCQLQRIQGLAFYKHLSDIFKGEPAALLPDS 120  
QY 121 PMEOLHTSLGLSOLLQPEDHPRETQOMPSLSSSQOWRPLRSKILRSLOAFLAIAARV 180  
|||||  
Db 121 PMEOLHTSLGLSOLLQPEDHPRETQOMPSLSSSQOWRPLRSKILRSLOAFLAIAARV 180  
QY 181 FAHGAATLTLEPLVPTA 196  
|||||  
Db 181 FAHGAATLTLEPLVPTA 196  
RESULT 2  
US-09-122-443-2  
; Sequence 2, Application US/09122443  
; Patent No. 6060284  
; GENERAL INFORMATION:  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/122,443  
; FILING DATE: 24-JUL-1998  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/053,765  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0758K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 189 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-122-443-2

Query Match 69.2%; Score 718.5; DB 3; Length 189;  
Best Local Similarity 74.6%; Pred. No. 2.5e-73;  
Matches 141; Conservative 14; Mismatches 33; Indels 1; Gaps 1;  
QY 1 MLDCAVITMLLPWVTQGLAVPRSSSDWNAQCQOLSRNLCMLAWNAHAPAGHMLNLR 60  
|||  
Db 1 MLGSRVAMLLLLPWTAGRAVPGGSPAWTQCQQLSKJCTTLAWSAPLVGHMD-LREE 59  
QY 61 EDEETKNNVPRIOCGDCDQGLKDNQSCQLQRIQGLAFYKHLSDIFKGEPAALLPDS 120  
|||||  
Db 60 GDEETNDVPHIQCGDCDQGLKDNQSCQLQRIQGLAFYKHLSDIFKGEPAALLPDS 119  
QY 121 PMEOLHTSLGLSOLLQPEDHPRETQOMPSLSSSQOWRPLRSKILRSLOAFLAIAARV 180  
|||||  
Db 120 PVAQLHASLLGSLLOLQPEGHWHWETQOIPSLSPSQWQRLLRKFILRSLOAFVAARV 179  
QY 181 FAHGAATLT 189  
|||||

Db 180 FAHGAATLS 188  
RESULT 3  
US-09-122-443-5  
; Sequence 5, Application US/09122443  
; Patent No. 6060284  
; GENERAL INFORMATION:  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/122,443  
; FILING DATE: 24-JUL-1998  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/053,765  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0758K1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 102 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-122-443-5  
Query Match 34.3%; Score 356; DB 3; Length 102;  
Best Local Similarity 72.3%; Pred. No. 9.1e-33;  
Matches 73; Conservative 8; Mismatches 20; Indels 0; Gaps  
QY 90 CLQRIQGLAFYKHLSDIFKGEPAALLPDS PMEOLHTSLGLSOLLQPEDHPRETQOMP 149  
|||||  
Db 2 CLQRIHQGLVFEYKELGLSDIFTGEPSLHPDGSVGLHSLGLRQLLOPEGHWHWETQTP 61  
QY 150 SLSSSQOWRPLRSKILRSLOAFLAIAARVFAHGAATLT 190  
|||||  
Db 62 SPSPSOPWQRLLRKLRSLOAFVAARVFAHGAATLSQ 102  
RESULT 4  
US-09-499-148-5  
; Sequence 5, Application US/09499148  
; Patent No. 6461604  
; GENERAL INFORMATION:  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.  
; APPLICANT: YU, HSIAANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1

```
; CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-499-148-5

Query Match
Best Local Similarity 10.8%; Score 112; DB 4; Length 162;
Matches 39; Conservative 22; Mismatches 50; Indels 30; Gaps 6;

QY 59 EEEDE-----ETKNNVPRIOCGCDPQGLKDNQSFCLQRIROGLAFYKHLLD--S 107
Db 27 EKNDCEKSKETLAENKLNLPKMEKDGCFQSGF--NQAICLIKTAGLLEYIYLDLQ 84
QY 108 DIFKGEPAALLPDSPEQLHTSLGLSLLQ-----PEDHPRETQOMPSSLSQQWQ 158
Db 85 NEFEGN-----QETVMELQSSIRTLQILKEKIAGLITTPATH---TDMLEKMQSSNEW 136
QY 159 RPLRSKILRSLOAFLAIAAR 179
Db 137 KNAKVIIILRSLENFLQFSLR 157

RESULT 5
US-09-122-443-13
; Sequence 13, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazaan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Egwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-13

Query Match
10.8%; Score 112; DB 3; Length 184;
```

```
Best Local Similarity 27.7%; Pred. No. 7.9e-05;
Matches 39; Conservative 22; Mismatches 50; Indels 30; Gaps 6;

QY 59 EEEDE-----ETKNNVPRIOCGCDPQGLKDNQSFCLQRIROGLAFYKHLLD--S 107
Db 49 EKNDCEKSKETLAENKLNLPKMEKDGCFQSGF--NQAICLIKTAGLLEYIYLDLQ 106
QY 108 DIFKGEPAALLPDSPEQLHTSLGLSLLQ-----PEDHPRETQOMPSSLSQQWQ 158
Db 107 NEFEGN-----QETVMELQSSIRTLQILKEKIAGLITTPATH---TDMLEKMQSSNEW 158
QY 159 RPLRSKILRSLOAFLAIAAR 179
Db 159 KNAKVIIILRSLENFLQFSLR 179
```

```
RESULT 6
US-09-499-148-2
; Sequence 2, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USC1
; CURRENT APPLICATION NUMBER: US/09/499,148
; CURRENT FILING DATE: 2000-02-07
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-499-148-2
```

```
Query Match
Best Local Similarity 10.0%; Score 104; DB 4; Length 162;
Matches 37; Conservative 23; Mismatches 54; Indels 24; Gaps 5;

QY 59 EEEDE-----ETKNNVPRIOCGCDPQGLKDNQSFCLQRIROGLAFYKHLLD--S 107
Db 27 EKNDCEKSKETLAENKLNLPKMEKDGCFQSGF--NQAICLIKTAGLLEYIYLDLQ 84
QY 108 DIFKGEPAALLPDSPEQLHTSLGLSLLQ-----DHPRETQOMPSSLSQQWQ 161
Db 85 NEYEGNQENVRD-----LRKNIRTLQILKOKIADLITTPATNTDLLEKMQSSNEW 139
QY 162 LRSKILRSLOAFLAIAAR 179
Db 140 KIILIRNLLENFLQFSLR 157
```

```
RESULT 7
US-09-499-148-3
; Sequence 3, Application US/09499148
; Patent No. 6461604
; GENERAL INFORMATION:
; APPLICANT: SOMERS, WILLIAM
; APPLICANT: STAHL, MARK L.
; APPLICANT: SEEHRA, JASBIR S.
; APPLICANT: XU, GUANG-YI
; APPLICANT: MCCONAGH, THOMAS E.
; APPLICANT: YU, HSIANG-AI
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6
; FILE REFERENCE: 50657-05278USC1
```

; CURRENT APPLICATION NUMBER: US/09/499,148  
; PRIOR FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-09-499-148-3

Query Match 9.9%; Score 103; DB 4; Length 166;  
Best Local Similarity 24.8%; Pred. No. 0.00071;  
Matches 38; Conservative 28; Mismatches 55; Indels 32; Gaps 6;  
QY 52 GHMNLREEDEDE-----ETKNNVPRIQEDGCDPQGLKDNSQFCQIRQGL 98  
Db 16 KGISALKKCMNDYKCEDEKLAENNLPLKAEKDCGFCQSGF--NQETCLTRITTTGL 73  
QY 99 AFYKHLDD--SDIFKGPALLPDSPMEOQLHTSLGLSOLLQPEDHPRETQOMP-----149  
Db 74 QEFQIYLFQDKYEGD-----EENAKSVYVSTNVLQLKLRGKNQDEVITIPVPTVEVG 128  
QY 150 ---SLSSQWQRPRLRSKILRSLOAFLATAAR 179  
Db 129 LOAKLOSQEEWLRHTTHLTLRLEDFLOFSLR 161

RESULT 8  
US-09-499-148-9  
; Sequence 9, Application US/09499148  
; Patent No. 6461604  
; GENERAL INFORMATION:  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.  
; APPLICANT: YU, HSIANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1  
; CURRENT APPLICATION NUMBER: US/09/499,148  
; CURRENT FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 9  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Sus scrofa domestica  
US-09-499-148-9

Query Match 9.6%; Score 100; DB 4; Length 166;  
Best Local Similarity 25.0%; Pred. No. 0.0015;  
Matches 39; Conservative 22; Mismatches 57; Indels 38; Gaps 5;  
QY 52 GHMNLREEDEDE-----ETKNNVPRIQEDGCDPQGLKDNSQFCQIRQGL 98  
Db 16 KGISARKKCEKYEKCEKNSKEVLAENNLPLKAEKDCGFCQSGF--NQETCLMRTITGL 73  
QY 99 AFYKHLDD--SDIFKGPALLPDSPMEOQLHTSLGLSOLLQPEDHPRETQOMPES---150  
Db 74 VEFQIYLDYLOKYESKNKN-----VEAVQISTKALIQTLRQKGNPKDPKATTPNPTT 125  
QY 151 -----LSSSQWQRPRLRSKILRSLOAFLATAAR 179  
Db 126 NAGLLDKLQSONEWKMKTKILLILRSLEDFLOFSLR 161

RESULT 9

US-09-499-148-7  
; Sequence 7, Application US/09499148  
; Patent No. 6461604  
; GENERAL INFORMATION:  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.  
; APPLICANT: YU, HSIANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1  
; CURRENT APPLICATION NUMBER: US/09/499,148  
; CURRENT FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-499-148-7  
Query Match 9.2%; Score 96; DB 4; Length 166;  
Best Local Similarity 25.5%; Pred. No. 0.0044;  
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;  
QY 35 OLSRNLCLAWNNAHAPAGHMNLLREEDEETKNN--VPRIQEDGCDPQGLKDNSQFCQ 92  
Db 19 EMRKELC-----NGNSDC--MN-----NDALAEENLKLPEIQRNDGCVQTY--NQEICLL 66  
QY 93 RIRQGLAFYKHLDD-----SDIFKGPALLP-----DSPMEQLHTSL--GLSQ 134  
Db 67 KISSGLLEYHVSLEYMKNNLKNKDKARVLQRDTETLIHIFNQEVKDLHKVILPTPTISN 126  
QY 135 LLOPEDHPRETQOMPESLSSQWQRPRLRSKILRSLOAFLATAAR 179  
Db 127 ALLTD-----KLESQEWLRTKTIQFILKSLEEFKAVTLR 161

RESULT 10  
US-09-122-443-14  
; Sequence 14, Application US/09122443  
; Patent No. 6060284  
; GENERAL INFORMATION:  
; APPLICANT: Bazan, J. Fernando  
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/122,443  
; FILING DATE: 24-JUL-1998  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/053,765  
; FILING DATE: 25-JUL-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0758K1



```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-14

Query Match          9.2%; Score 96; DB 3; Length 188;
Best Local Similarity 25.5%; Pred. No. 0.0052;
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGDCDPQGLKDNSQFCLQ 92
Db 41 EMRKELC-----NGSDC--MN-----NDDALAENNLKLPETQIRNDGCVQYGY--NQEICLL 88
QY 93 RIRQGLAFYKHLLD-----SDIFKGEPAALLP-----DSPMEQLHTSLL--GLSQ 134
Db 89 KISSGLLEVSHVLEYMKNNLKDKKARVLQRTDTETLIHFNFQEVKDLHKIVLPTPISN 148
QY 135 LLOPEDHPRETQOMPSSSSQQWQRPRLRSKILRSQAFLAIAAR 179
Db 149 ALLTD-----KLESQEWLRTKTIQFILKSLEEFKLVTLR 183

RESULT 11
US-08-097-869-8
; Sequence 8, Application US/08097869
; Patent No. 6204364
; GENERAL INFORMATION:
; APPLICANT: Todaro, George J.
; APPLICANT: Rose, Timothy M.
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,869
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,178
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24455-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 211 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-097-869-8
```

```
Query Match          9.2%; Score 96; DB 4; Length 211;
Best Local Similarity 25.5%; Pred. No. 0.0062;
Matches 42; Conservative 24; Mismatches 57; Indels 42; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCEGDCDPQGLKDNSQFCLQ 92
Db 64 EMRKELC-----NGSDC--MN-----NDDALAENNLKLPETQIRNDGCVQYGY--NQEICLL 111
QY 93 RIRQGLAFYKHLLD-----SDIFKGEPAALLP-----DSPMEQLHTSLL--GLSQ 134
Db 112 KISSGLLEVSHVLEYMKNNLKDKKARVLQRTDTETLIHFNFQEVKDLHKIVLPTPISN 171
QY 135 LLOPEDHPRETQOMPSSSSQQWQRPRLRSKILRSQAFLAIAAR 179
Db 172 ALLTD-----KLESQEWLRTKTIQFILKSLEEFKLVTLR 206

RESULT 12
US-08-209-182C-6
; Sequence 6, Application US/08209182C
; Patent No. 5545537
; GENERAL INFORMATION:
; APPLICANT: Skelly, Susan M.
; APPLICANT: Tackney, Charles T.
; APPLICANT: Snouwaert, John N.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ImClone Systems Incorporated
; STREET: 180 Varick Street
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10014
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/209,182C
; FILING DATE: 10-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/724,698
; FILING DATE: 02-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Feit, Irving N.
; REGISTRATION NUMBER: 28,601
; REFERENCE/DOCKET NUMBER: SKE-1-PD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-645-1405
; TELEFAX: 212-645-2054
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-209-182C-6

Query Match          8.9%; Score 92.5; DB 1; Length 186;
Best Local Similarity 25.7%; Pred. No. 0.013;
Matches 36; Conservative 22; Mismatches 61; Indels 21; Gaps 4;

QY 53 HMNLLREEDEETKNNVPRIQCEGDCDPQGLKDNSQFCLQRIQGLAFYKHLSDIFPK 112
Db 50 NMSESSKEALAEANLNLPKMAEKDCFGSGF--NETCLVKIITG-----LLFEFVYLE 101
QY 113 EPALLPDSPMEQ---LHTSLILGLSOLLQPE-----DHPRETQOMPSSSSQQWQR 159
Db 102 IPPNRFESSEQARAVQMSTKVLQFLOKAKNLDLITTPDPTTNASILLTKLAQNQWLQ 161
```

QY 160 PLLRSKILRSLOAFIAAR 179  
Db 162 DMTHILRSKFELQSSLR 181

## RESULT 13

PCT-US92-05612-6  
; Sequence 6, Application PC/TUS9205612  
; GENERAL INFORMATION:  
; APPLICANT: Skelly, Susan M.  
; APPLICANT: Tackney, Charles T.  
; APPLICANT: Snouwaert, John N.  
; APPLICANT: Fowlkes, Dana M.  
; TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ImClone Systems Incorporated  
; STREET: 180 Varick Street  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 10014  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/05612  
; FILING DATE: 19920702  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Felt, Irving N.  
; REGISTRATION NUMBER: 28,601  
; REFERENCE/DOCKET NUMBER: SKE-1-PT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-645-1405  
; TELEFAX: 212-645-2054  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 186 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US92-05612-6

Query Match 8.9%; Score 92.5; DB 5; Length 186;  
Best Local Similarity 25.7%; Pred. No. 0.013;  
Matches 36; Conservative 22; Mismatches 61; Indels 21; Gaps 4;

QY 53 HNNLLREEDEETKNNVPRIQCDGCDPQGLKDNSQFCLORIQGLAFYKHLSDIFKG 112  
Db 50 NWSSESKALANNLNPVKMAEKDCQSGF--NEETCLVKIITG-----LLEFEVYLE 101  
QY 113 EPALLPDSPMEO---LHFTSLGLSLOLQPE-----DHPRETQOMPSSSSQWQR 159  
Db 102 IPPNRFESSEQARAVOMSTKVLQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLQ 161  
QY 160 PLLRSKILRSLOAFIAAR 179  
Db 162 DMTHILRSKFELQSSLR 181

## RESULT 14

US-09-499-148-6  
; Sequence 6, Application US/09499148  
; GENERAL INFORMATION:  
; Patent No. 6461604  
; APPLICANT: SOMERS, WILLIAM  
; APPLICANT: STAHL, MARK L.  
; APPLICANT: SEHRA, JASBIR S.  
; APPLICANT: XU, GUANG-YI  
; APPLICANT: MCCONAGH, THOMAS E.

; APPLICANT: YU, HSIANG-AI  
; APPLICANT: HONG, JIN  
; TITLE OF INVENTION: CRYSTALLINE IL-6 AND MODELS OF THE MOLECULAR STRUCTURE OF IL-6  
; FILE REFERENCE: 50657-05278USC1  
; CURRENT APPLICATION NUMBER: US/09/499,148  
; CURRENT FILING DATE: 2000-02-07  
; PRIOR APPLICATION NUMBER: US 08/841,035 AND 60/024,115  
; PRIOR FILING DATE: 1997-4-28 AND 1996-8-16  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 6  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Rattus norvegicus  
US-09-499-148-6

Query Match 8.8%; Score 91; DB 4; Length 166;  
Best Local Similarity 24.5%; Pred. No. 0.016;  
Matches 39; Conservative 27; Mismatches 63; Indels 30; Gaps 9;

QY 35 QLSRNLCLAWNAHAPAGHMNLLREEDEETKNN--VPRIQCDGCDPQGLKDNSQFCQLQ 92  
Db 19 ENRKELC---NGSDC--MN---SDDLSENNLKLPFIQRNDGCFQTGY--NQEICLL 66  
QY 93 RTRQGLAFYKHLDD-----SDIFKGEPAALLPDSPMEOHLTSLGLSLOLQPEDH---PR 143  
Db 67 KICSGLLEFEFYLEFVKNNLQDNKKDKARVIOSTETLVHI----FKOEIKDSYKIVLPT 122  
QY 144 ETQQO---MPSLSSQOWORPLLRSKILRSLOAFIAAR 179  
Db 123 PTSNALLMEKLESQKRWLRTKTIQLILKALEFLKVTWR 161

## RESULT 15

US-09-487-792-14  
; Sequence 14, Application US/09487792  
; Patent No. 6433145  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Keratinocyte Derived Interferon  
; FILE REFERENCE: PF482Pl  
; CURRENT APPLICATION NUMBER: US/09/487,792  
; CURRENT FILING DATE: 2000-01-20  
; EARLIER APPLICATION NUMBER: 60/093,643  
; EARLIER FILING DATE: 1998-07-21  
; EARLIER APPLICATION NUMBER: PCT/US99/16424  
; EARLIER FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 14  
; LENGTH: 212  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-487-792-14

Query Match 8.6%; Score 89; DB 4; Length 212;  
Best Local Similarity 22.0%; Pred. No. 0.038;  
Matches 39; Conservative 27; Mismatches 71; Indels 40; Gaps 7;

QY 15 WVTQGLAVPRSSSPDWAOCQQLSRNLCLAWNAHAPAGHMNLLREEDEETKNNVPRIQC 74  
Db 59 YILDGISALRKET-----CNK--SNWCESSKEALA-----ENNINLPKXAK 97  
QY 75 EDGCDPQGLKDNSQFCLORIQGLAFYKHLDD--SDIFKGEPAALLPDSPMEOHLTSLGL 132  
Db 98 EDGCFQSGF--NEETCLVKIITGLLEFEVYLEVLQNRFFS-----EQARAVOMSTKVL 150  
QY 133 SLLQPE-----DHPRETQOMPSSSSQWQRPLLRSKILRSLOAFIAAR 179  
Db 151 IQFLQKKAKNLDAITTPDPTTNASLLTKLQANQWLQDMTHILRSKFELQSSLR 207

Search completed: November 20, 2002, 12:00:13

Job time : 13.2182 secs

---

